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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:58:25 ; Search time 12.48 Seconds
(without alignments)
102.779 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257

Perfect score: 302

Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGSPPPARGSTGCD 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 152146

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	27.5	15	US-08-221-583-56	Sequence 56, Appl
2	83	27.5	15	PCT-US95-04018-56	Sequence 56, Appl
3	82	27.2	15	US-08-221-583-58	Sequence 58, Appl
4	82	27.2	15	PCT-US95-04018-58	Sequence 58, Appl
5	81	26.8	15	US-08-221-583-57	Sequence 57, Appl
6	81	26.8	15	US-08-221-583-62	Sequence 62, Appl
7	81	26.8	15	PCT-US95-04018-57	Sequence 57, Appl
8	81	26.8	15	PCT-US95-04018-62	Sequence 62, Appl
9	80	26.5	15	US-08-221-583-55	Sequence 55, Appl
10	80	26.5	15	US-08-221-583-59	Sequence 59, Appl
11	80	26.5	15	PCT-US95-04018-55	Sequence 55, Appl
12	80	26.5	15	PCT-US95-04018-59	Sequence 59, Appl
13	79	26.2	15	US-08-221-583-61	Sequence 61, Appl
14	79	26.2	15	PCT-US95-04018-61	Sequence 61, Appl
15	78	25.8	15	US-08-221-583-60	Sequence 60, Appl
16	78	25.8	15	PCT-US95-04018-60	Sequence 60, Appl
17	69	22.8	15	US-08-221-583-54	Sequence 54, Appl
18	69	22.8	15	PCT-US95-04018-54	Sequence 54, Appl
19	59	19.5	45	US-08-361-920-19	Sequence 19, Appl
20	59	19.5	45	US-08-479-939-19	Sequence 19, Appl
21	59	19.5	45	US-08-483-432-19	Sequence 19, Appl
22	58	19.2	54	US-08-471-780C-44	Sequence 44, Appl
23	58	19.2	54	US-08-467-282B-44	Sequence 44, Appl
24	58	19.2	54	US-08-471-282A-44	Sequence 44, Appl
25	58	19.2	54	US-08-466-710C-44	Sequence 44, Appl
26	58	19.2	54	US-08-468-739C-44	Sequence 44, Appl
27	55	18.2	15	US-08-221-583-53	Sequence 53, Appl

28 55 18.2 15 5 PCT-US95-04018-53 Sequence 53, Appl
29 55 18.2 46 3 US-08-856-074A-39 Sequence 39, Appl
30 55 18.2 48 6 5171885-7 Patent No. 5171885
31 55 18.2 48 6 5518916-7 Patent No. 5518916
32 53.5 17.7 37 3 US-08-814-052-37 Sequence 37, Appl
33 53.5 17.7 37 3 US-08-812-829-29 Sequence 29, Appl
34 52.5 17.4 21 5 PCT-US92-10432-1 Sequence 1, Appl
35 52.5 17.4 22 1 US-08-443-542-43 Sequence 43, Appl
36 52.5 17.4 22 3 US-08-765-469-43 Sequence 43, Appl
37 50.5 16.7 53 6 5422248-4 Patent No. 5422248
38 50 16.6 16 1 US-08-366-591-15 Sequence 15, Appl
39 49.5 16.4 33 1 US-08-237-716-11 Sequence 11, Appl
40 49.5 16.4 40 1 US-08-099-354-11 Sequence 1, Appl
41 49.5 16.4 40 2 US-08-288-059-7 Sequence 7, Appl
42 49.5 16.4 41 1 US-08-361-920-13 Sequence 13, Appl
43 49.5 16.4 41 1 US-08-479-939-13 Sequence 13, Appl
44 49.5 16.4 41 1 US-08-483-432-13 Sequence 13, Appl
45 49 16.2 16 1 US-08-471-033-47 Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-221-583-56
; Sequence 56, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221.583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-221-583-56

Query Match 27.5%; Score 83; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 HLPQPVSTRSQHTQP 29

Db 1 HLPQPVSTRSQHTQP 15

RESULT 2

PCT-US95-04018-56
; Sequence 56, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-56

Query Match 27.5%; Score 83; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 HLPQPVSTRSQHTOP 29
Db 1 HLPQPVSTRSQHTOP 15
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RESULT 3
US-08-221-583-58
; Sequence 58, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania

COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-58

Query Match 27.2%; Score 82; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 SQHTOPTPEPTAPS 38
Db 1 SQHTOPTPEPTAPS 15
|||||

RESULT 4
PCT-US95-04018-58
; Sequence 58, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-58

Query Match 27.2%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 SQTQTPPEPSTAPS 38
|||||
DB 1 SQTQTPPEPSTAPS 15

RESULT 5
US-08-221-583-57
Sequence 57, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-57

Query Match 26.8%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 STRSQHTQTPPEPST 35
|||||
DB 1 STRSQHTQTPPEPST 15

RESULT 6
US-08-221-583-62
Sequence 62, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-62

Query Match 26.8%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 APSTSFLPLPMGSPSP 50
|||||
DB 1 APSTSFLPLPMGSPSP 15

RESULT 7
PCT-US95-04018-57
Sequence 57, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-57

Query Match 26.8%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 STRSQHTQTPPEPST 35
Db 1 STRSQHTQTPPEPST 15

RESULT 8
PCT-US95-04018-62
Sequence 62, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-62

Query Match 26.8%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 APSTSFLLPMGPSP 50
Db 1 APSTSFLLPMGPSP 15

RESULT 9
US-08-221-583-55
Sequence 55, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25.mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-55

Query Match 26.5%; Score 80; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAVHLPQPVSTRSQH 26
Db 1 GAVHLPQPVSTRSQH 15


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RESULT 11
PCT-US95-04018-55
; Sequence 55, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04018
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/221,580
: FILING DATE: 01-APR-1994
: APPLICATION NUMBER: US 08/221,580
: FILING DATE: 01-APR-1994
: APPLICATION NUMBER: US 08/221,583
: FILING DATE: 01-APR-1994
: APPLICATION NUMBER: US 08/221,581
: FILING DATE: 01-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Deluca, Mark
: REGISTRATION NUMBER: 33,229
: REFERENCE/DOCKET NUMBER: CCOR-0232
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 55:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PCT-US95-04018-55
:
: Query Match 26.5%; Score 80; DB 5; Length 15;
: Best Local Similarity 100.0%; Pred. No. 0.0077;
: Matches 15; Conservative 0; Mismatches 0; Indels
:
: QY 12 GAVHLPQPVSTRSQH 26
:
: Db 1 GAVHLPQPVSTRSQH 15
:
:
: RESULT 12
: PCT-US95-04018-59
: Sequence 59 Application PC/TUS9504018
: GENERAL INFORMATION:
: APPLICANT: Heavner, George A.
: APPLICANT: Kruszynski, Marian
: APPLICANT: Mervic, Miljenko
: APPLICANT: Weber, Robert W.
: TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
: NUMBER OF SEQUENCES: 76
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
: ADDRESSEE: Norris
: STREET: One Liberty Place 46th Floor
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19403
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04018
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/221,580
: FILING DATE: 01-APR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/221,583
: FILING DATE: 01-APR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/221,581

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; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-59

Query Match      26.2%; Score 80; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQTPPEPSTAPSTSF 41
Db 1 TQTPPEPSTAPSTSF 15

RESULT 13
US-08-221-583-61
; Sequence 61, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-61

Query Match      26.2%; Score 79; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches, 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 PSTAPSTSFLLPMGP 47
Db 1 PSTAPSTSFLLPMGP 15

US-08-221-583-61
; Sequence 60, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
```

```
RESULT 14
PCT-US95-04018-61
; Sequence 61, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-61

Query Match      26.2%; Score 79; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 PSTAPSTSFLLPMGP 47
Db 1 PSTAPSTSFLLPMGP 15

RESULT 15
US-08-221-583-60
; Sequence 60, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
```

STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-60

Query Match 25.8%; Score 78; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 TPEPSTAPSTSFLLP 44
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Db 1 TPEPSTAPSTSFLLP 15

Search completed: February 12, 2002, 13:00:17
Job time: 112 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:45:58 ; Search time 19.28 Seconds
(without alignments)
1821.394 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVDPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	100.0	461	1 A35356	tumor necrosis fac
2	1512	61.3	474	2 B38634	tumor necrosis fac
3	1477	59.8	459	2 I48854	gene murine tumour
4	381.5	15.5	349	2 D72175	G2R protein - vari
5	379.5	15.4	348	2 T28623	hypothetical prote
6	379.5	15.4	349	2 T36858	gene G4R protein -
7	360.5	14.6	326	1 G0V2ML	T2 protein - myxom
8	341.5	13.8	435	2 I54182	tumor necrosis fac
9	328	13.3	325	2 B43692	T2 protein - rabbi
10	317.5	12.9	277	2 A60771	B-cell activation
11	238.5	10.5	305	2 A46476	B cell-associated
12	251.5	10.2	416	1 JN0006	nerve growth facto
13	241	9.8	595	2 A42086	CD30 antigen precu
14	229.5	9.3	271	2 S12783	OX40 antigen precu
15	223.5	9.1	272	2 I48700	gene ox40 protein
16	219.5	8.9	493	2 J05486	membrane glycoprot
17	217	8.8	277	2 I37552	OX40 homolog - hum
18	210	8.5	427	1 G0HUN	nerve growth facto
19	198	8.0	461	2 J04302	tumor necrosis fac
20	197	8.0	256	2 B32393	T-cell antigen 4-1
21	197	8.0	425	1 A36431	nerve growth facto
22	191.5	7.8	454	1 G0MST1	tumor necrosis fac
23	185.5	7.5	461	1 G0RTT1	tumor necrosis fac
24	185	7.5	255	2 I38426	lymphocyte activat
25	183.5	7.4	455	1 G0HUT1	tumor necrosis fac
26	166.5	6.7	1367	1 S48478	glucan 1,4-alpha-g
27	165	6.7	770	2 T51024	related to C2H2 zi
28	161.5	6.5	1203	2 T17415	mycellial surface a
29	161	6.5	1372	2 T25933	hypothetical prote

30 159.5 6.5 2232 2 T34434
31 158 6.4 1274 2 T42017
32 156.5 6.3 383 2 T46707
33 154.5 6.3 1428 2 T08852
34 153.5 6.2 3507 2 T34513
35 150 6.1 801 2 T29018
36 148.5 6.0 1032 2 T34433
37 148 6.0 327 2 A46484
38 147 6.0 438 2 T31889
39 147 6.0 600 2 S07638
40 145 5.9 742 2 I37225
41 144 5.8 314 2 I37383
42 143.5 5.8 324 2 JC2395
43 143 5.8 534 2 T39903
44 143 5.8 3942 2 T42730
45 142 5.8 1151 2 T18535

ALIGNMENTS

RESULT 1
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular A
A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SNL>
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAAS9929.1; PID:g189186
R:Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195,'R',197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular A
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAAB19824.1; PID:g235649
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons A
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor A
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40;65-69;136-141;300-306 <LOE>

hypothetical prote
cysteine rich prot
proteophosphoglyca
lustrin A - Califo
hypothetical prote
hypothetical prote
hypothetical prote
apoptosis-mediati
hypothetical prote
spore coat protein
leucocyte antigen
FAS soluble protei
Fas antigen precu
serine-rich protei
Bassoon protein -
high molecular mas

E;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215
A:Accession: B35010
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: I38094; MUID:95121934
A:Accession: I38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:g666044; PID:g825701
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:l25914; OMIM:l91191
A:Map position: 1p36.2-1p36.2
A:Introns: 26/3
A:Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 2

B38634
tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chan, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A:Reference number: A38634; MUID:91187885
A:Accession: B38634
A:Molecule type: mRNA
A:Residues: 1-474 <LEW>
A:Cross-references: GB:M60469; NID:gl99827; PIDN:AAA39752.1; PID:gl99828
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J. Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors
A:Reference number: A40254; MUID:91246158
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:gl99827; PIDN:AAA39752.1; PID:gl99828
R:Kisssoneghis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor
A:Reference number: S54816
A:Accession: S54816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KIS>
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F:40-77/Domain: NGF receptor repeat homology <NG1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 61.3%; Score 1512; DB 2; Length 474;
Best Local Similarity 63.0%; Pred. No. 1.7e-79;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

Qy 1 MAPVAVMAALAVGLELWAAHALPAQVAFYPAPEPGSTCRL-REYYDQTAQMCCSKGSP 59
Db 1 MAPAALWALVELQLWATHTYPAQVLLTPYKPEGYEQISOEYYDRKAQMCACKCPP 60

Qy 60 GOHAKVFCPTKTDVTCDCSEDSTYTQLWNWVPECLSCGSCSSDOVETQACTREQNRICT 119
Db 61 GOYVHFCKNTSDTVTCADCEASMYTQVNWQFRTCLGSSSCTTDQVEIRACTKQNRVCA 120

Qy 120 CRPGWYCALSKOEG-CRLCAPLRKCPGFCVGARPGTETSDVVKPCAPGTSTNTSSTDI 178
Db 121 CEAGRYCALTKHSGSCRCQMRSLKCGPGFVGASSRAPNGNVLCRACAPGTSDTTSSTDV 180

Qy 179 CRPHOICNVVALPGNMAIDAVCTSTPTRSMAPCAVHLPOPVSTRSQHTQTPTPEPSTAPS 238
Db 181 CRPHICSLIALPGNASTDAVCAPEPTLSAIPRTLIVSQPEPTRSQPLDQEPGFSQTP- 239

Qy 239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGTALGLLIIGVNCVIMTVQVKKPKLCLORE 297
Db 240 -SILTSLSGTPIEQSTKGGISLPIGLIVGTVSLGLEMLGLVNCIILVQRKKPKSCLQRD 298

Qy 298 AKVPHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQPAQGV-EAS 356
Db 299 AKVPHVPDEKSDAVGLEQOQHLLITAPSSSSSSLESSASAGDRRAPPGGHFQARYMAEQ 358

Qy 357 GAGEARASTGSSDPGGHGTQVNVTCIVNVCSSDRSHSSCSQASSTMGTDSSPSSEP 416
Db 359 GFQEARASRISDSSHSGHGTHTVNVTCIVNVCSSDRSHSSCSQASATVGPDPDAKPSAP 418

Qy 417 KDEQVPFKEECAFRSQLETPTETLLGSTEEKPLPLGVDPDAGMKPS 461

C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992

A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:q456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, V.M.; submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: G4R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 15.4%; Score 379.5; DB 2; Length 349;
Best Local Similarity 37.6%; Pred. No. 5.3e-15;
Matches 79; Conservative 24; Mismatches 86; Indels 21; Gaps 7;
Qy 31 PYAPEGSTCLREYDQTAQMCCKSCPGOHAKVCTKTSDTVCDSCEDSTVTQLWNV 90
Db 24 PTP-PNGCKDTEY--KRNLCCLCPGPGTYASRLCDSTNTQCTPCGSGTISRNNHL 80
Qy 91 PECLSGSRCSDDQVETQACTREQNRICTCRPGWYCALSKQEGCRICAPLRKCRPGFGVA 150
Db 81 PACLSGCRGNSQVETRSCTNTHNRICECPGYCYLLKGGSGCKACVSTQTKGIGYGV 140
Qy 151 RPTGTSDDVCKPCAPGTFSTNTSSDTCRPHQICNVVAIPGNA--SMDAVCT-----ST 203
Db 141 -GHTSGVDICSPGFGTYSHTVSSADKCEP-----VPNTFNVIDEITLYPVNDT 191
Qy 204 SPTRSNAPGAVH--LPQPVSTRSQHTQPTP 231
Db 192 SCTRTTTTGLSEILFTSELTITMNTDCNP 221

RESULT 7
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991

A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>

A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g3323310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 360.5; DB 1; Length 326;
Best Local Similarity 36.9%; Pred. No. 6.1e-14;
Matches 75; Conservative 29; Mismatches 86; Indels 13; Gaps 6;

Qy 31 PYAPEGSTCLREYDQTAQMCCKSCPGOHAKVCTKTSDTVCDSCEDSTVTQLWNV 90
Db 20 PYGADRGR-CRGNDY--EKDGLCTCCPPGYSVSLRCLGPGSDTVGSPCKNETFTASTNHA 76

Qy 91 PECLSGSRCSDDQVETQACTREQNRICTCRPGWYCALSKQEGCRICAPLRKCRPGFGVA 150
Db 77 PACVSCRGRCCTGHLSSESQCDKTRDVCDSAGNYCLLKRGEGCRICAPKCPAGYGV 136

Qy 151 RPTGTSDDVCKPCAPGTFSTNTSSDTCRPHQICNVVAIPGN--ASMDAVCTSTSPTRS 208
Db 137 -GHTRTGDVLCTKCPRTYSDAVSSTETCT--SSFNYISVEFNLYPVNDTSCITTA---- 189

Qy 209 MAPGAVHLPQPVSTRSQHTQPTP 231
Db 190 -GPNEVVKTSFVSVLNHTDCDP 211

RESULT 8
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaifanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
A:Reference number: I54182; MUID:93252381
A:Accession: I54182
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C:Genetics:
A:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 13.8%; Score 341.5; DB 2; Length 435;
Best Local Similarity 29.1%; Pred. No. 9.7e-13;
Matches 120; Conservative 45; Mismatches 141; Indels 107; Gaps 25;

Qy 2 APVAVWAALAVGL-ELWAAA--HALPAQVATPYAPEGSTCR--LREYDQTAQMCCKSK 56
Db 9 APGLAWGPLVLGLGALLAASQPAVP-----PYASE-NQTCRDQEKYEYEPQHRICCSR 61
Qy 57 CSPGOHAKVCTKTSDTVCDSCEDSTVTQLWNVPECLSGSRCSDDV-----ETQACTR 112
Db 62 CPPGTIVYSAKCSIRDTVCATCAENSYNEHWNLYLTICQLCR---PCDPVMGLEETAPCHS 118

Qy 113 EQNRICTRCPGWYCALSKQEGCRICAPLRKCRPGFGVARGPTSETSDVV-----CKPCAP 166
Db 119 KRKTQCRQCPGMFCAAWALE-CTHCELLSDCPG-----TEAEKDEKGVGNHVCVCKA 172
Qy 167 GTFENNTSSDTCRPHQICN-----VVAIPGNASMDAVCTSTSPTRSMAPG-----AV 214
Db 173 GHFONTSSPSARCQPHTRCENQGLVEAPGTAQSDTTC--KNPLEPLPPEMSTMLLAV 230
Qy 215 HLPQP-----VST-----RSQHTQTPPTSTPSTFLL---PMGPSP-PAGSG----- 254

Db 231 LLPLAFFLLLATVFCIMKWS-----HPSLCKLGLSLLKRRPQGGPNPVAGSWPEPPKA 283
QY 255 -----TGDFAFPVLGVITAGLLIIGVNVNCVIMTVQKKKPLCLQREAKV 300
Db 284 HPYFDPVLQPLPIISGDVS-PVS--TGLPAAPVLEAGVPQ-----QQSPDLDTRE--- 330
QY 301 PHL-PADKARGTQGPQQHLLITAPSSSSSSLESSASALDRAPTRNQPOAPG 352
Db 331 POLEPGEQSOVAHGTNGIHV-----TCGSMITITGNIYINCPVLGGPPGPG 376

RESULT 9
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Virolgy 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103
A:Accession: B43692
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homolog
F:64-105/Domain: NGF receptor repeat homolog <NG2>
F:106-147/Domain: NGF receptor repeat homolog <NG3>

Query Match 13.3%; Score 328; DB 2; Length 325;
Best Local Similarity 36.9%; Pred. No. 4.3e-12;
Matches 66; Conservative 28; Mismatches 71; Indels 14; Gaps 6;
QY 31 PVAPBPGSTCLREYDQPAQMCCKSCPGQAKVFTKTSDFVCDSCEDSTVQLNWW 90
Db 20 PYSNQKG-CGGHDY--EKDGLCCASCHPEFYASRLCGGNSFVCSPECDGTFTASTNHA 76
QY 91 PECLSCGSCSSDQVETQACTREQNRICRPGWYCALSKQEGCRCLCAPLRCRPGFGVA 150
Db 77 PACVSCRGPTCHLSESQPCDRTHRVNCSTGNYCLLKGQNGCRICAPQTKCPAGYGV 136
QY 151 RPTETSDVWCKPAPGTFSTNTSDICRPHQICNVAI-----PGNASMDAVCTSTS 204
Db 137 -GHTRAGDTLCEKPPHTYSDLSPTERCSTS--FNYISVGFNLYPVN---ETSCITTA 189

RESULT 10
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CRAA43045.1; PID:g29851
R:Braesch-Andersen, S.; Paulie, S.; Kobo, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40

A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homolog
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 317.5; DB 2; Length 277;
Best Local Similarity 26.7%; Pred. No. 1.5e-11;
Matches 92; Conservative 32; Mismatches 124; Indels 97; Gaps 11;
QY 23 LPAQVA-----FTPYAPEPGSTCLREYDQPAQMCCKSCPGQAKVFTKTSDFVCD 77
Db 4 LPLQCVLWGCLLTAVHPEPTACREKQVLYNS--QCCSLCQPGOKLVSDCTETETECLP 61
QY 78 CEDSTYTLQNLNWPEC-----LSCGSCSSDQVETQACTREQNRICRPGWYCALSK 130
Db 62 CGESEFLDTWNRETHCHQHKYCDPNLGRVQ-----OKGTSETDTICTCEEHCT--- 112
QY 131 QEGCRLCAPLRCRPGFGVAPGTTSDVCKPCAPGTFSTNTSDICRPHQICN---- 186
Db 113 SEACESCVLHRKSCSPGFGVKQIATGVSDTICEPCVPVGFNSVSAFEKCHPWTSCETKDL 172
QY 187 VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPOPVSTRSQHTQPTPEPSTAPSTSELLPMG 246
Db 173 VVQAGTKNTDVVCGPQDRLRAL----- 195
QY 247 PSPPAEGSTGDFALVGLVGTALGLLIIGVNCVIMTVQKKKPLCLQREAKVPH---- 302
Db 196 -----VVPIIFGILFAILLVL-----VFIKKVAKKP-----TNKAPHPKOE 232
QY 303 -----LPAD-KARTQGPQHQHLLITAPSSSSSSLESSASALDRR 341
Db 233 PQEINFDDPLPGSNTAAPVQETHLGHQCPVTDGKESRISVQERQ 277

RESULT 11
A6476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:g1553058
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, 'LV' <GR>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A:Experimental source: BALB/c, liver
A:Note: sequence extracted from NCBI backbone (NCBIP:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homolog
C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 10.5%; Score 258.5; DB 2; Length 305;
Best Local Similarity 22.8%; Pred. No. 3.8e-08;
Matches 87; Conservative 37; Mismatches 142; Indels 115; Gaps 14;

QY 5 AVNALAVGLLWAAHALPAQVAFYAPPEGSTCLRLREYYDQTAQMCCKSPGQHAQ 64
DB 9 ALMGCLLTAVHLGCV-----TCSDKQYLHD--GQCCDLCPGSRLLT 48
QY 65 VFTKTSDDTCDSCEDSTYTQLNWVPECLSCGSCSSDQ---VETQACTREQNRICTR 121
DB 49 SHCTALEKTOCHPCDSEFEQAQWREIRCHO--HRHCEPNOGLRVKKEG--TAESDTVCCK 106
QY 122 PGWYCALSKGEGRLCLAPLRKCRFGVARGTETSDDVCKPCAPGTFSTSTDCICRP 181
DB 107 EGQCHT---SKDCACAAHQHPCIPGFGVMEMATETTDVCHPCPGVFGFSNOSSLFKCY 163
QY 182 HQICN-----VVAIPGNASMDAVCTSTPTSRMAPGAVHLPOPVSTRSQHTQPTPEPSTAP 237
DB 164 WTSCEDKNLEVLQKGTSTQNVICLKSRRAL----- 195
QY 238 STSFLLPMGSPPAEGSTGDFALPGLVIGVTALGLLIIGVWNCVIMTQVKKPLCLQRE 297
DB 196 -----LVIPVWMLITITFGVFL-----YIKKVKKP---KDN 225
QY 298 AKVPHLPADK-----ARCTQGEQOHLITAPSSSSSSLESSASALDR----- 340
DB 226 EMPLP--PAARRQDQEMEDYVGHNTAAPVQETHGCPVTOEDKESRISVOERQVDSI 283
QY 341 --RAPTRNPQAPGVASGAG 359
DB 284 ALRPPGLN----PCTATGGDG 300

RESULT 12

JN0006

N:Alternate names: NGF receptor, low affinity precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JN0006; A60504

R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid
Neuron 2, 1123-1134, 1989

A:Title: Structure and developmental expression of the nerve growth factor receptor in t

A:Reference number: JN0006; MUID:90186579

A:Accession: JN0006

A:Molecule type: mRNA

A:Residues: 1-416 <LAR>

A:Experimental source: embryonic chick brain

R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.

Dev. Biol. 137, 287-304, 1990

A:Title: Structure and developmental expression of the chicken NGF receptor.

A:Reference number: A60504; MUID:90152140

A:Accession: A60504

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of

C:Comment: This protein is thought to form a high-affinity receptor when it associates w

C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-416/Product: nerve growth factor receptor #status predicted <MAT>

F:21-239/Domain: extracellular #status predicted <EXT>

F:24-57/Domain: NGF receptor repeat homology <NG1>

F:59-100/Domain: NGF receptor repeat homology <NG2>

F:101-139/Domain: NGF receptor repeat homology <NG3>

F:141-181/Domain: NGF receptor repeat homology <NG4>

F:189-237/Region: serine/threonine-rich

F:240-261/Domain: transmembrane #status predicted <MEM>

F:262-416/Domain: intracellular #status predicted <INT>
F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 251.5; DB 1; Length 416;
Best Local Similarity 25.1%; Pred. No. 1.3e-07;
Matches 89; Conservative 48; Mismatches 164; Indels 53; Gaps 16;

QY 23 LPAQVAFYAPPEGS--TCRLREYYDQTAQMCCKSPGQHAQVFTKTSDDTCDSCSD 80
DB 5 VFLLLLPAGPTWGSKEKCLTKMY--TTSGECKKACNLGEGVVQPC-GVNTQVCEPCLD 61
QY 81 S-TYQLNWNVPECLSCGSCSSDQVETQACTREQNRICTRCPGWYCALSKQEGRLCAP 139
DB 62 SVTYSDTVSATPEKPC-TQCGLHSMSPACVESDADVCAVGYF----QDELSGSCKE 116
QY 140 LRKCRPGCVARGTETSDDVCKPCAPGTFSTSTSDICRPHQICNVVAIPGNASMDAV 199
DB 117 CSICEVGFGLMFPFCDSDQPTVCEGPEGTFDEANFVDPCLPCTICE-----ENEMVKE 171
QY 200 CTSTSTPT--RSMAP--GAVHLPOPVSTRSQHTQPTPEP-----STAPSTSFLLPM 245
DB 172 CTATSDAECRLDHPKWTHTPSLAGSDS-----PEPITRDPTNTEGMATTLADIVTVM 225
QY 246 GPSP--AEGSTGDFALPVGLIIVGTALGLLIIGVWNCVIMTQVKKPLCLQREAKVPHLP 304
DB 236 GSSQPVWSRGATADNLIPVCSI---LAAVVGLVAYIAF---KRWNSCKQKQGANRP 278
QY 305 ADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNOQAPGVASGA 358
DB 279 VNQ---TPSPEKEL-----HSDSGISYDSQSLHDQPPNQSTQGPAPKGDGS 323

RESULT 13

A42086

CD30 antigen precursor - human

N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000

C:Accession: A42086

R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.

Cell 68, 421-427, 1992

A:Title: Molecular cloning and expression of a new member of the nerve growth factor

A:Reference number: A42086; MUID:92154659

A:Accession: A42086

A:Molecule type: mRNA

A:Residues: 1-595 <DUR>

A:Cross-references: GB:M83554; NID:g180095; PIDN:AAA51947.1; PID:g180096

A:Experimental source: HUT-102 cell line

A>Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBI:82090)

C:Genetics:

A:Gene: GDB:CD30; D1S166E

A:Cross-references: GDB:I31547; OMIM:153243

A:Map position: lp36-lp36

C:Superfamily: NGF receptor repeat homology

C:Keywords: glycoprotein; growth factor receptor; transmembrane protein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-38/Domain: extracellular #status predicted <EXT>

F:384-407/Domain: transmembrane #status predicted <TMM>

F:408-595/Domain: intracellular #status predicted <CYT>

F:101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.8%; Score 241; DB 2; Length 595;
Best Local Similarity 22.0%; Pred. No. 7.1e-07;

Matches 113; Conservative 41; Mismatches 183; Indels 176; Gaps 17;

QY 11 AVGLELWAAHALPAQVAFYAPPEGSTC--RLREYYDQTAQMCCKSPGQHAQVFT 68

DB 7 ALGLLFLGALRAFPODRPFE-----DTCHGNPSSHYYDKAVRRCYCPCMGFLPPTQQCP 59

QY 69 KTSDDTVCDSCEDSTYTQLNWVPECLSCGSCSSDQVETQACTREQNRICTRCPGWYCAL 128

Db 60 QRPTDCRKOCEPDYLL---DEADRCACVTCSDRDLLVEKTPCAWNSRVCRCRPMFCST 116
Qy 129 SKQECRLCAPLRKCRPGFVGARPGTETSDVCKPCAPG----- 167
Db 117 SAVNSCARCFFHSCVCPAGMIVKPEPGTAOKNTVCEPASPGVPACASPENCKEPPSSGTTIPQ 176
Qy 168 -----TFSTNTT----- 173
Db 177 AKPTVPSTATSSASTWVPVGRGTRLAQEAASKLTRAPDSPSSVGRPSSDRGLSPTQPCPEG 236
Qy 174 -----SSTDCRPHQICNVVAIPG 192
Db 237 SGDCRKOCEPDYLLDEAGRCTACVSCSRDLDLEKTPCAWNSRVCRCRPMFCST 296
Qy 193 NASMDAVCTSTPTSRMAPGAVHLFQ-----PVSTRSQHTQPTPE-----PST 235
Db 297 -----CARCVYPICAAETVTKPDMAEKDTTFEAPPLGTQPD-CNPTPEGEAPAST 348
Qy 236 APSTSFLL-----LPMGSPPP-AGEGSGDFALPVLGVGTALGLLIGVVNCVIMTQ 286
Db 349 SPTQSLLDVDSQASKLPIPTSPALVSSSTGKPVLDAGPVLFWILVVLVVVGSSAFLLCH 408
Qy 287 VKKKPLCLQREAKVPHL---PADKARGTQGPQEQHLLITAPSSSSSSLESSASALDRRAPT 344
Db 409 ---RRACRKRIRQKHLCLCPVQ---TSQPKLE-LVDSRPRSSSTQLRSGASVTEPVAEE 460
Qy 345 R---NOQPAGVEASGAGBARASTGSSDSPGG 374
Db 461 RGLMSOPLMETCHSVGAAYLE-SLPLQDASPAG 492

RESULT 14

SI2783
Ox40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: SI2783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC Ox40 antigen of activated CD4 positive T lymphocyte
A:Reference number: SI2783; MUID:90214614
A:Accession: SI2783
A:Molecule type: mRNA
A:Residues: 1-271 <RES>
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C:Superfamily: CD27 antigen; NGF receptor repeat homolog
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/domain: signal sequence #status predicted <SIG>
F:20-271/product: Ox40 antigen #status predicted <MAT>
F:211-235/domain: transmembrane #status predicted <TM>

Query Match 9.3%; Score 229.5; DB 2; Length 271;
Best Local Similarity 27.1%; Pred. No. 1.5e-06;
Matches 79; Conservative 28; Mismatches 88; Indels 97; Gaps 14;

Qy 6 VW-----AALAVGLELWAAHALPAQVATPYAPEGSGTCLREYDYD--QTAQWCCSKCS 58
Db 3 VWQOPTAFLLGLSL-----GVTVKNCVKDTPSGHKCCRECC 42
Qy 59 PGHAKVFTKTSDTVCDSCSDSTYTQLMNW--VPECLSGSGSCSDQVETQACTREONR 116
Db 43 PGHGVSRCDHTRDTVCHPCETGTFYNEAVNYDTCKOCTQCNHRSGSEL--KQNCPTTPT 100
Qy 117 ICTCRPGWYCALSKQEGCRCLCAPLRKCRPGFVGARPGTETS---DVVCKPCAPGTFSTNT 173
Db 101 VCOCRPG-----TQPRQDSSHLKGVDCVPCPGHFS--P 132
Qy 174 SSTDCRPHQICNV-----VAIPGNASMDAVCTSTPTRMAPGAVHLFPQVSTRSQHT-- 227
Db 133 GSNQACKPWTNCTLSGKQIRHPASNSLDTVCEDRS-----LLATLLWETQRTTF 181

Qy 228 OPTPEPSTA-----PSTSFLL-PMGSPPPAEGSGTGFALPVLGVGVTA 270
Db 182 RPTVPSTTVPRTSQLPSTPTLVAPEGPA-----FAVILGLGLGLLA 224

RESULT 15

I48700
gene ox40 protein - mouse
N:Alternate names: Ox40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:g312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat Ox
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-14 'G', 16-272 <RES>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: Ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homolog

Query Match 9.1%; Score 223.5; DB 2; Length 272;
Best Local Similarity 27.0%; Pred. No. 3.3e-06;
Matches 88; Conservative 32; Mismatches 97; Indels 109; Gaps 19;

Qy 6 VW-----AALAVGLELWAAHALPAQVATPYAPEGSGTCLREYDYDQTAQWCCSKCSPG 60
Db 3 VWQOPTAFLLGLSL-----NCVKHTY--PSGHKCCRECCQ 45
Qy 61 QHAKVFTKTSDTVCDSCSDSTYTQLMNW--VPECLSGSGSCSDQVETQACTREONR 118
Db 46 HGMVSRCDHTRDTLCHPCETGTFYNEAVNYDTCKOCTQCNHRSGSEL--KQNCPTTQDTVC 103
Qy 119 TCRPGWYCALSKQEGCRCLCAPLRKCRPGFVGARPGTETS---DVVCKPCAPGTFSTNTSS 175
Db 104 RCRPG-----TQPRQDSSGYKLGVDVCPGPHFS--PGN 135
Qy 176 TDCRPHQICNV-----VAIPGNASMDAVCTSTPTRMAPGAVHLFPQVSTRSQHTQ-PT 230
Db 136 NQACKPWTNCTLSGKQIRHPASNSLDAVCE-----LATLLWETQRTPT 181
Qy 231 PEPSTA-----PSTSFLLPMGSPPPA---EGSGDFALPVLGVGVTA-LGLLIGVV 279
Db 182 FRPTIVGSTTVPRTSEL-----PSPPTLVTEGPA--FAVILGLGLGLLAPLTVLL---- 231
Qy 280 NCVIMTQVKKKPLCLQREA-KVPHLP 304
Db 232 -----ALYLLRKAWRPLNTP 246

Search completed: February 12, 2002, 12:48:26
Job time: 148 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:48:04 ; Search time 13.25 Seconds
(without alignments)
1275.659 Million cell updates

Title: US-09-800-909-2

Perfect score:

Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVDPDAGMKPS 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB sea length: 0

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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post-processing: Minimum March 08

Fast processing: Minimum Match 0% Maximum Match 100%

Maximum March 1998
Listing first 45 summaries

Database : SwissProt 39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2462	99.8	461	1	TNR2_HUMAN	P20333 homo sapien
2	1532	61.3	474	1	TNR2_MOUSE	P25119 mus musculus
3	379.5	15.4	349	1	VC32_VARV	P34015 variola vir
4	360.5	14.6	326	1	VT2_MTXVL	P29825 myxoma viru
5	341.5	13.8	435	1	TNRC_HUMAN	P36941 homo sapien
6	328	13.3	325	1	VT2_SFVKA	P25943 shope fibro
7	317.5	12.9	277	1	CD40_HUMAN	P25942 homo sapien
8	317	12.8	415	1	TNRC_MOUSE	P50284 mus musculu
9	259	10.5	289	1	TR14_HUMAN	Q92956 homo sapien
10	252.5	10.2	283	1	CD40_MOUSE	P27512 mus musculu
11	251.5	10.2	416	1	NGFR_CHICK	P18519 gallus gall
12	242.5	9.8	269	1	CD40_BOVIN	Q28203 bos taurus
13	241	9.8	595	1	CD30_HUMAN	P28908 homo sapien
14	229.5	9.3	271	1	OX40_RAT	P15725 rattus norv
15	223.5	9.1	272	1	OX40_MOUSE	P47741 mus musculu
16	217	8.8	277	1	OX40_HUMAN	P43489 homo sapien
17	210	8.5	427	1	NGFR_HUMAN	P08138 homo sapien
18	199	8.1	471	1	TNR1_BOVIN	O19131 bos taurus
19	198	8.0	461	1	TNR1_PIG	P05055 sus scrofa
20	197	8.0	256	1	41BB_MOUSE	P20334 mus musculu
21	197	8.0	425	1	NGFR_RAT	P07174 rattus norv
22	191.5	7.8	454	1	TNR1_MOUSE	P25118 mus musculu
23	185.5	7.5	461	1	TNR1_RAT	P22934 rattus norv
24	185	7.5	255	1	41BB_HUMAN	Q07011 homo sapien
25	183.5	7.4	455	1	TNR1_HUMAN	P19438 homo sapien
26	166.5	6.7	1367	1	AMTH_YEAST	P08640 saccharomyc
27	152	6.2	323	1	FASA_BOVIN	P51867 bos taurus
28	148	6.0	327	1	FASA_MOUSE	P25446 mus musculu
29	147	6.0	600	1	SP96_DICDI	P14328 dictyosteli
30	146.5	5.9	687	1	VS41_GIALA	P2127 giardia lam
31	144.5	5.9	835	1	CD97_HUMAN	P48960 homo sapien
32	144	5.8	332	1	FASA_PIG	Q07736 sus scrofa
33	143.5	5.8	324	1	FASA_RAT	Q63199 rattus norv

ALIGNMENTS

RESULT	1
TNR2_HUMAN	
ID	TNR2_HUMAN STANDARD; PRT; 461 AA.
AC	P20333;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DE	20-AUG-2001 (Rel. 40, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE	BINDING PROTEIN 2) (TFPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
GN	TNFRSF1B OR TNFR2 OR TNFR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90260639; PubMed=2160731;
RA	Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA	Dower S.K., Cosman D., Goodwin R.G.;
RT	"A receptor for tumor necrosis factor defines an unusual family of
RL	cellular and viral proteins.";
RL	Science 248:1019-1023(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91045991; PubMed=2172983;
RA	Kohn T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA	Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT	"A second tumor necrosis factor receptor gene product can shed a
RT	naturally occurring tumor necrosis factor inhibitor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96299745; PubMed=8661109;
RA	Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA	Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA	Brodeur G.M.;
RT	"Physical mapping and genomic structure of the human TNFR2 gene.";
RL	Genomics 35:94-100(1996).
RN	[4]
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX	MEDLINE=90349572; PubMed=2166946;
RA	Heiler R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA	Ringold G.M.;
RT	"Complementary DNA cloning of a receptor for tumor necrosis factor
RT	and demonstration of a shed form of the receptor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN	[5]
RP	SEQUENCE OF 27-31.
RX	MEDLINE=90110215; PubMed=2153136;
RA	Engelmann H., Novick D., Wallach D.;
RT	"Two tumor necrosis factor-binding proteins purified from human
RT	urine. Evidence for immunological cross-reactivity with cell surface
RT	tumor necrosis factor receptors.";
RL	J. Biol. Chem. 265:1531-1536(1990).
RN	[6]
RP	SEQUENCE OF 23-40:65-69; 136-141; 300-306 AND 346-362.

RX MEDLINE=91056048; PubMed=2173696;
RA Loetscher H., Schlaefer E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RN J. Biol. Chem. 265:20131-20138(1990).
RN (7)
RP CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Penica D., Lam V.T., Mize N.K., Weber R.F., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RJ J. Biol. Chem. 267:21172-21178(1992).
RJ (8)
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2";
RL Nature 398:533-538(1999).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
CC WYETH-AYERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrelinfo.com/".
CC -----
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CC -----
DR EMBL; M32315; AAC59929.1; -;
DR EMBL; M35857; AAC63262.1; -;
DR EMBL; U52165; AAC50622.1; -;
DR EMBL; U52156; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAC36755.1; -;
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR PDB; 1CA9; 12-APR-99.
DR MIM; 191191; -;
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461
FT DOMAIN 23 257 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 288 461 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 141 141 R -> P (IN REF. 4).
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
FT CONFLICT 363 363 A -> T (IN REF. 4).
SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 99.8%; Score 2462; DB 1; Length 461;
Best Local Similarity 99.8%; Pred. No. 3.9e-136;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVWAALVGLLELWAAHAALPAQVATPYAPPEGSCRLREYDYDQTAQMCCSKSPG 60
DB 1 MAPVAVWAALVGLLELWAAHAALPAQVATPYAPPEGSCRLREYDYDQTAQMCCSKSPG 60

QY 61 QHAKVCTKTSTVDCSDSTVTLWNWVPECLSCGSCSSDQVETQACTREQNRCTC 120
DB 61 QHAKVCTKTSTVDCSDSTVTLWNWVPECLSCGSCSSDQVETQACTREQNRCTC 120

QY 121 RFGWCALSKQEGCRICAPLRKCRPGFVGARFGTETSDVCKPCAPGTETSTTSSTDIR 180
DB 121 RFGWCALSKQEGCRICAPLRKCRPGFVGARFGTETSDVCKPCAPGTETSTTSSTDIR 180

QY 181 PHQICNVVAIPGNASNDVACTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPESTAPSTS 240
DB 181 PHQICNVVAIPGNASNDVACTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPESTAPSTS 240

QY 241 FLLPMGPPAPBEGSTGDFALPVGLIVGVLTALGLLIIGVYVNCVIMTOVKKPLCLQREKV 300
DB 241 FLLPMGPPAPBEGSTGDFALPVGLIVGVLTALGLLIIGVYVNCVIMTOVKKPLCLQREKV 300

QY 301 PHLPADKARGTQGPQEQHLLITAPSSSSSSLESSSASALDRRAPTRNQPAQVGEASGAGE 360
DB 301 PHLPADKARGTQGPQEQHLLITAPSSSSSSLESSSASALDRRAPTRNQPAQVGEASGAGE 360

QY 361 ARASTGSSDSPGGHGTQVNVVTCIVNVCSSSDHSSQCSSQASSTMGDTSSSPSESPEKDEQ 420
DB 361 ARASTGSSDSPGGHGTQVNVVTCIVNVCSSSDHSSQCSSQASSTMGDTSSSPSESPEKDEQ 420

QY 421 VPFSKECAFRSOLPETTLGSTEKPLPLGVDPAGMKPS 461
DB 421 VPFSKECAFRSOLPETTLGSTEKPLPLGVDPAGMKPS 461

RESULT 2
TNR2_MOUSE
ID TNR2_MOUSE STANDARD: PRT: 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DR	EMBL; X69198; CAA49137.1; -.
DR	EMBL; X67117; CAA47540.1; -.
DR	PIR; D36858; D36858.
DR	PIR; S35987; S35987.
DR	PIR; S46888; S46888.
DR	HSSP; P19438; INCF.
DR	InterPro; IPR001368; TNFR_C6.
DR	Fam; PF00020; TNFR_C6; 2.
DR	ProDom; PD000771; TNFR_C6; 1.
DR	SMART; SM00208; TNFR; 2.
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.
KW	Repeat..
FT	DOMAIN 31 108
FT	REPEAT 31 66
FT	REPEAT 67 108
SQ	SEQUENCE 349 AA; 338189 MW; D45D40B5C6E780F CRC64;

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EMBL; M95181; AAA45632.1; -. DR	EMBL; A23729; CAA01688.1; -. DR	PIR; A40566; GOVZML. DR	HSSP; P19438; 1TNR. DR	InterPro; IPR001368; TNFR_C6. DR	Pfam; PF00020; TNFR_C6; 2. DR	ProDom; PD000771; TNFR_C6; 1. DR	SMART; SM00208; TNFR; 3. DR	PROSITE; PS00652; TNFR_NGFR_1; 2. DR	PROSITE; PS00650; TNFR_NGFR_2; 2. DR	Receptor; Glycoprotein; Repeat; Signal. KW	POTENTIAL. FT	CHAIN 1 16 FT	SHAIN 17 326 FT	DOMAIN 27 186 FT	REPEAT 27 62 FT	REPEAT 63 104 FT	REPEAT 105 147 FT	REPEAT 148 186 FT	CARBOHYD 66 66 FT	CARBOHYD 181 181 FT	CARBOHYD 205 205 FT	CARBOHYD 238 238 FT	SEQUENCE 326 AA; 35208 MW; ABBF027E947293FF CRC64; SQ
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transcribed sequences derived from a somatic cell hybrid.";
[2]
RT Genomics 16:214-218(1993).
RN FUNCTION.
RP MEDLINE=94225209; PubMed=81711323;
RX Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; L04270; AAA36757.1; .
CC HSSP; P25942; 1CDF.
CC
CC MIM; 600979; .
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 211 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;

Query Match 13.8%; Score 341.5; DB 1; Length 435;

Best Local Similarity 29.1%; Pred No. 2.4e-13;
Matches 120; Conservative 45; Mismatches 141; Indels 107; Gaps 25;

QY 2 APVAVNAALAVGL-ELWAAA--HALPAQVAFTPYAPEPGSTCR--LREYDQTAQMCCKS 56

Db 9 AFGLAWPLVLGLFGLAASQPAVE-----PYASE-NQTCRQKEKYEYPOHRCSSR 61

QY 57 CSPGQIAKVCFTKSTVDCSDSTSTYQLNWNVPCLSGSCSSDQV-----ETQACTR 112

Db 62 CPPGTVVSACRSIRDTVCATCAENSYNHWNLYTICQLCR---PCDPVNGLEEIAPECTS 118

QY 113 EQNRICTCRPGWYCALSKOEGCRCLAPLRCRPGFVGARPGTETSDVV-----CKPCAP 166

Db 119 KRKTCRCOPGFMFCAAWALE-CTHCELLSDCPPG-----TEAEKDKVKGNNHCVPCKA 172

QY 167 GTFSTNTSSDIDICRPHOICN---VVAIPGNASMDAVCTSTSPTRSMAPG-----AV 214
Db 173 GHFQNTSSPSARCQPHTRCENOGVLEAPGTAQSDTTC--KNPLELPPEMSGTMMLAV 230
QY 215 HLPQP-----VST-----RSQHTQPTPEPSTAPSTFLL---PMGPSP-PAEGS----- 254
Db 231 LLPLAPFLLLATVFCISWKS-----HPSLCRKGLSLLKRRPQEGPNPVAGSWEPPKA 283
QY 255 -----TGDFALPVLGLIVGVTALGLLIIGVNVVIMTVQVKKKPLCLQREAKV 300
Db 284 HPYFPDLVQPLLPISGDVS-PVS--TGLPAAPVLEAGVPQ-----QQSPDLDTRE--- 330
QY 301 PHL-PADKARGTQGPQEQHLLITAPSSSSSSLESSASALDRRAPTRNOPOAPG 352
Db 331 PQLEPGSQSVAHGTNGIHV-----TGGSMITGNIYIYNGPVLGGPPGP 376
RESULT 6
VT2_SFVKA
ID VT2_SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2]
RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; M17433; .; NOT_ANNOTATED_CDS.
DR EMBL; A23727; CAA01687.1; .
DR PIR; B43692; B43692.
DR HSSP; P19438; ITNR.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.


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CC EMBL; X60592; CAA3045.1; -.
CC PIR; S04460; S04460.
CC PDB; 1CDF; 01-APR-97.
CC MIM; 109535; -.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153
FT CARBOHYD 180 180
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Query Match 12.9%; Score 317.5; DB 1; Length 277;
Best Local Similarity 26.7%; Pred. No. 3.8e-12;
Matches 92; Conservative 32; Mismatches 124; Indels 97; Gaps 11;
QY 23 LPAQVA-----FYPAYEPGSGTCLREYYDQTQAMCCSKCSPGQHAKVFTKTSDFVCD 77
Db 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 LPLQCVLWGCLLFAVHPEPTACRQGYKLINS--QCCSLCQPGQKLVSDCTEFTECLP 61
QY 78 CEDSTYTLQNNWVPEC-----LSCGSRCSBQVETQACTRQNRICTCRPGWYCALSK 130
Db 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 CGESEFLDTWNRETHCHQHKYCDPNGLRVQ-----QKGTSETDICTCEGWHCT--- 112
QY 131 QEGCRICAPLRKCPGFGVARGPQTETSDVVKCPAPGTFSNTTSSDIDCRPHQICN--- 186
Db 113 SEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFSPNVSSAFKCHPWTSCETKDL 172
QY 187 VVAIPGNASMDVACTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTFLLPMG 246
Db 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
173 VVOAGTNTKDDVVCGPQDRURAL----- 195
QY 247 PSPPAEGSGTGFALPGLVIGVFTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPH--- 302
Db 196 -----VVIPIFGILFAILLVL-----VFIKKVAKP-----TNKAPHKQE 232
QY 303 -----LPAD-KARGTGQPEQHLLITAPSSSSSSLESSASALDRR 341
Db 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
233 PQEINFPDDLPGSNTAAPVQETLHGCPQVTDGKESRISVQERQ 277
RESULT 8
TNRC_MOUSE
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;

```

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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:56:45 ; Search time 23.73 Seconds
(without alignments)
177.926 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257

Perfect score: 302

Sequence: 1 TSTSPTRSMAPGAVHLQPV.....STSFLLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 288181

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68.5	22.7	47	21 AAB56300	Human secreted pro
2	67.5	22.4	49	19 AAW59911	Amino acid sequenc
3	59	19.5	45	12 AAR13261	Linking B region #
4	58	19.2	54	15 AAR49722	Sequence of a pept
5	58	19.2	54	15 AAR49536	Camel Ig 2-heavy c
6	56.5	18.7	41	20 AAY01285	Peptide encoded by
7	56	18.5	47	22 AAM19336	Peptide #5770 enco
8	56	18.5	47	22 AAM32132	Peptide #6169 enco
9	55	18.2	46	20 AAW88522	Amphotropic hyperv
10	55	18.2	52	22 AAB61193	Human INTERCEPT 21
11	54.5	18.0	55	21 AAB42690	Human ORFX ORF2454

12	54	17.9	21	9 AAP81606	Sequence of human
13	54	17.9	36	21 AAY65289	Human 5' EST relat
14	54	17.9	50	22 AAM17997	Peptide #4431 enco
15	54	17.9	50	22 AAM30506	Peptide #4543 enco
16	54	17.9	50	22 AAM05637	Peptide #4319 enco
17	53.5	17.7	37	18 AAW26641	H. insoliens family
18	52.5	17.4	21	14 AAR37992	Heavy chain hinge
19	52	17.2	50	18 AAW35739	Mucin peptide MUC1
20	52	17.2	51	18 AAW31697	Mucin peptide MUC1
21	51.5	17.1	55	22 AAM33030	Peptide #7067 enco
22	51	16.9	40	17 AAR88860	Peptide targeted
23	51	16.9	40	22 AAM18924	Peptide #5358 enco
24	51	16.9	40	22 AAM31492	Peptide #5529 enco
25	51	16.9	43	20 AAY49096	Amino acid sequenc
26	51	16.9	50	22 AAM20331	Peptide #6785 enco
27	51	16.9	50	22 AAM34632	Peptide #8669 enco
28	50	16.6	16	17 AAR99693	IgA protease speci
29	50	16.6	19	20 AAW99681	Human IgA1 hinge r
30	50	16.6	21	20 AAY42923	Core peptide in th
31	50	16.6	25	19 AAW64623	Human IgA1 CH2 reg
32	50	16.6	25	19 AAW61595	Human IgA1 CH2 rec
33	50	16.6	25	20 AAW85774	IgA1 CH2 region pr
34	50	16.6	52	21 AAG03497	Human secreted pro
35	50	16.6	52	22 AAG74844	Human colon cancer
36	49.5	16.4	40	16 AAR68002	Mucin repeat seque
37	49.5	16.4	40	19 AAW72703	Human mucin peptid
38	49.5	16.4	41	12 AAR15255	Linking B region #
39	49	16.2	27	9 AAP80541	Sequence of portio
40	49	16.2	35	15 AAR49650	Sequence of hinge
41	49	16.2	35	15 AAR49529	Camel 2-chain Ig h
42	49	16.2	40	19 AAW54873	Carcinoma-associat
43	49	16.2	46	20 AAY01284	Peptide encoded by
44	49	16.2	47	21 AAB38081	Fragment of human
45	48.5	16.1	34	20 AAY03809	Lck binding active

ALIGNMENTS

RESULT 1
AAB56300
ID AAB56300 standard; Protein; 47 AA.
XX AAB56300;
XX AC
XX AC
DT 13-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 99 SEQ ID NO:394.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virocidic;
KW fungicide; ophthalmological; gene therapy; pathological condition;
KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;
KW cerebrovascular disorder; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; skin aging; food additive; preservative.
XX
OS Homo sapiens.
XX
PN WO200070042-A1.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12788.
XX
PR 13-MAY-1999; 99US-0134068.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;
PI Duan RD, Florence KA, Soppet DR;

```

XX WPI; 2000-679828/66.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein -
XX used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; Page 1035; 1065pp; English.
XX
XX The polynucleotide sequences given in AAC99818 to AAC99977 encode the
XX human secreted proteins given in AAB56077 to AAB56362. Human secreted
XX proteins have activities based on the tissues and cells the genes are
XX expressed in. Examples of activities include: immunosuppressive;
XX antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
XX vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
XX virucide; fungicide; and ophthalmological. The human secreted
XX polynucleotides and proteins can be used to prevent, treat or ameliorate
XX a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
XX dogs, chickens or sheep. They are also used in diagnosing a pathological
XX condition or susceptibility to a pathological condition. Disorders which
XX are diagnosed or treated include autoimmune diseases e.g. rheumatoid
XX arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
XX liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
XX disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
XX e.g. Alzheimer's disease, infections caused by bacteria, viruses and
XX fungi and ocular disorders e.g. corneal infection. The proteins can also
XX be used to aid wound healing and epithelial cell proliferation, to
XX prevent skin aging due to sunburn, to maintain organs before
XX transplantation, for supporting cell culture of primary tissues, to
XX regenerate tissues and in chemotaxis. The proteins can also be used as a
XX food additive or preservative to increase or decrease storage
XX capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 47 AA;
XX
XX
XX Query Match 22.7%; Score 68.5; DB 21; Length 47;
XX Best Local Similarity 40.5%; Pred. NO. 3.1;
XX Matches 17; Conservative 3; Mismatches 17; Indels 5; Gaps 1
XX
XX QY 19 PVSTRSQHTQTPTE-----PSTAPSTSTLLPMGSPPAEGST 55
XX ||||| ||| | : : | | ||||| | :
XX 5 pvsctipgsptshathtpctspptpxshpsxpspatss 46
XX
XX RESULT 2
XX ID AAW59911 standard; peptide: 49 AA.
XX XX
XX AC AAW59911;
XX XX
XX DT 20-NOV-1998 (first entry)
XX XX
XX DE Amino acid sequence of the mutanase enzyme PT box.
XX XX
XX KW Mutanase enzyme; PT box; alpha-1,3 glucoside bond; mutan; plaque;
XX KW bacteria; teeth.
XX XX
XX OS Bacillus sp.
XX XX
XX XX JP10201483-A.
XX XX
XX XX 04-AUG-1998.
XX XX
XX XX 01-OCT-1997; 97JP-0284362.
XX XX
XX XX 25-NOV-1996; 96JP-0314057.
XX XX
XX XX (LJOY ) LION CORP.
XX PA
XX XX
XX XX WPI; 1998-474495/41.
XX XX
XX Gene encoding a mutanase enzyme - used for prevention and removal

```

RESULT 4

AAR49722
 ID AAR49722 standard; peptide: 54 AA.
 AC AAR49722;
 DT 22-AUG-1994 (first entry)
 XX Sequence of a peptide which is part of the heavy (H) chain (CH3) of an
 DE immunoglobulin (Ig).
 DE Immunoglobulin; heavy chain; Camelid.
 KW Immunoglobulin; heavy chain; Camelid.
 XX Camelus dromedarius.
 OS Camelus dromedarius.
 XX WO9404678-A.
 PN 03-MAR-1994.
 PD 18-AUG-1993; 93WO-EP02214.
 PF 21-AUG-1992; 92EP-0402326.
 PR 21-MAY-1993; 93EP-0401310.
 XX (CAST/) CASTERMAN C.
 PA (HAME/) HAMERS R.
 XX Casterman C, Hamers R;
 PI WPI; 1994-083195/10.
 DR Immunoglobulins devoid of light chains - also processes for their
 XX preparation, and protein and nucleotide sequence encoding them.
 PT Claim 21; Page 65; 87pp; English.
 XX A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)
 CC polypeptide chains sufficient for the formation of a complete
 CC antigen binding site or several such chains. The Ig is devoid of
 CC light (L) polypeptide chains. The Ig may be obtd. from prokaryotic
 CC cells, esp. E. coli, by: cloning a DNA or cDNA sequence coding for
 CC the VH domain of an Ig devoid of L chains obtainable from e.g.
 CC lymphocytes of Camelids; recovering the cloned fragment after
 CC amplification using a 5' primer contg. an Xho site and a 3' primer
 CC contg. the Spe site having the sequence in AAQ44383; cloning the
 CC recovered fragment is a vector; transforming host cells; and
 CC recovering the expression product of the VH coding sequence.
 CC A nucleotide encoding the peptides in AAR49721-24 is claimed.
 XX
 SQ Sequence 54 AA;

Query Match 19.2%; Score 58; DB 15; Length 54;
 Best Local Similarity 31.6%; Pred. No. 38;
 Matches 12; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY 16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPPSPPAEG 53
 DB 9 ipqpqpkpqppqpqpkpqpkepectcpcpapellg 46

RESULT 5

AAR49536
 ID AAR49536 standard; peptide: 54 AA.
 AC AAR49536;
 DT 04-SEP-1994 (first entry)
 XX Camel Ig 2-heavy chain molecule (clone no. 72/79).
 DE Immunoglobulin; Ig; heavy chain; constant region; variable region;
 KW antibody engineering; IgG2; IgG3.

RESULT 6

AAY01285
 ID AAY01285 standard; Protein; 41 AA.

AC AAY01285;

DT 01-JUN-1999 (first entry)

DE Peptide encoded by HRGP gene cassette.

KW Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP;
 KW repetitive proline-rich protein; RPRP; arabino-galactan protein; ACP;
 KW glycopeptide; internal repeat.

OS Synthetic.

PN WO9903978-A1.

PD 28-JAN-1999.

PF 21-JUL-1998; 98WO-US15083.

PR 20-JUL-1998; 98US-0897556.

XX

OS Camelus dromedarius.

XX

FH Key Location/Qualifiers

FT Region 6..40

FT Region /note= "hinge region"

FT Region /note= "heavy chain variable region"

FT Region 41..54

FT Region /note= "heavy chain constant region"

XX

PN EP584421-A.

XX

PD 02-MAR-1994.

XX

PF 21-AUG-1992; 92EP-0402326.

XX

PR 21-AUG-1992; 92EP-0402326.

XX

PA (CAST/) CASTERMAN C.

XX

PA (HAME/) HAMERS R.

XX

PI Casterman C, Hamers R;

XX

DR WPI; 1994-067061/09.

XX

PT New isolated immunoglobulin molecules devoid of light polypeptide
 PT chains - consisting of heavy polypeptide chains only, obtd. from
 PT Camelid serum, for use as antibodies
 XX
 PS Disclosure; Page 19; 35pp; English.

XX

CC This 2-chain Ig molecule lacks any light chains. The Ig has
 CC e.g. improved solubility and aggregate much less than heavy chains
 CC of 4-chain Igs. The Igs can be used normally for e.g. diagnosis,
 CC therapy, in vaccines, for isolation and purification of antigens
 CC and in the production of anti-idiotypic antibodies.

XX

SQ Sequence 54 AA;

XX

Query Match 19.2%; Score 58; DB 15; Length 54;
 Best Local Similarity 31.6%; Pred. No. 38;

XX

Matches 12; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY

16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPPSPPAEG 53

DB

9 ipqpqpkpqppqpqpkpqpkepectcpcpapellg 46

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

Homo sapiens.

W0200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000WO-US086621.

31-MAR-1999; 99US-0127607.

02-APR-1999; 99US-0127636.

05-APR-1999; 99US-0127728.

30-MAR-2000; 2000US-0540763.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-602362/57.

N-PSDB; AAC76899.

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 11; Page 4083; 5507pp; English.

AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

Sequence 55 AA;

Query Match 18.0%; Score 54.5; DB 21; Length 55;

Best Local Similarity 38.3%; Pred. No. 85;

Matches 18; Conservative 1; Mismatches 17; Indels 11; Gaps 3;

QY 19 PVSTRSQHTQTPES-----TAPSTSFLLPMGPS---PPAEGSTG 56

Db 5 P\$grtprtptpypcphgdrllppsr--lpagpasafppaersrg 49

RESULT 12

AAP81606

ID AAP81606 standard; protein; 21 AA.

XX AAP81606;

AC AAP81606; (first entry)

DT 02-OCT-1990

DE Sequence of human immunoglobulin A1 (IgA1).

XX Human Cu/Zn superoxidisedismutase polymer; pSODCFISODHA1;

KW human immunoglobulin A1; hinge region; antiinflammatory agent;

XX Homo sapiens.

Key Location/Qualifiers

Region 1..20

FT /note="Hinge #1"

FT Protein 4..20

FT /note="IgA1"

XX EP283244-A.

PN 21-SEP-1988.

XX 15-MAR-1988; 88EP-0302244.

XX 16-MAR-1987; 87US-0026143.

PR (CHIR-) CHIRON CORP.

XX Hallewell RA, Mullenbach G;

XX WPI; 1988-265657/38.

DR P-PSDB; AAN80435.

PT Superoxidedismutase polymers having extended in vivo life - comprising superoxidisedismutase monomers covalently coupled by polypeptide spacers

Example; Page 5; 21pp; English.

XX A Cu/Zn superoxide dismutase (SOD) polymer of SOD units of at least 2 SOD monomers covalently coupled, carboxy terminus to amino terminus, to each other by a polypeptide spacer of at least 3 amino acids is claimed. The polymers are of formula

(SOD monomer - IgA - SOD monomer)_x or

(SOD monomer - IgA - SOD monomer - IgA - SOD monomer)_x

IgA - a 10-100 amino acid long segment of an immunoglobulin hinge region x = 2-4

XX AAN80435 was used to make pSODCFISODHA1 encoding bacterial expression spacer-linked human SOD monomers. AAN80435 encodes human IgA1 hinge region beginning at AA residue 226 to avoid the Cys 225 residue with BamHI and NcoI sites at its ends. The SOD polymers have an extended

XX circulatory life and retain the activity of SOD. The cloning and sequencing of human SOD (hSOD) cDNA and prodn. of hSOD in bacteria and yeast are described in EP-138111.

XX Sequence 21 AA;

Query Match 17.9%; Score 54; DB 9; Length 21;

Best Local Similarity 48.0%; Pred. No. 36;

Matches 12; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 16 LPQPVSTRSQHTQTPPEPSTAPSTS 40

Db 1 laqpvps----tbptpsbptps 21

RESULT 13


```

XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488897/53.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX PS Claim 27; SEQ ID No 30775; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders.
XX SQ Sequence 50 AA;

Query Match 17.9%; Score 54; DB 22; Length 50;
Best Local Similarity 40.0%; Pred. No. 87;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 27 TQPTPEPSTAPSTSFLLPMGSPSPA 51
Db 17 tippppasstppmnlplpppspps 41

```

Search completed: February 12, 2002, 12:59:58
Job time: 193 sec

01-OCT-1996 (Rel. 34, Last sequence update)
 01-OCT-1996 (Rel. 34, Last sequence update)
 01-NOV-1997 (Rel. 35, Last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
 GN LTBR OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CVB; TISSUE=Lung;
 RC MEDLINE=96072804; PubMed=7594541;
 RX Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakanura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; U29173; AAA68964.1; -;
 DR EMBL; L38423; AAB00846.1; -;
 DR EMBL; U30798; AAA81334.1; -;
 DR HSSP; P25942; 1CDF.
 DR MGD; MGI:104875; ltrb.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 3.
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
 FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 224 244 POTENTIAL.
 FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 213 4 X TNFR-CYS.
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 170 TNFR-CYS 3.
 FT REPEAT 171 213 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 160 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;
 Query Match 12.8%; Score 317; DB 1; Length 415;
 Best Local Similarity 24.9%; Pred. NO. 6e-12;
 Matches 119; Conservative 50; Mismatches 166; Indels 142; Gaps 22;
 QY 7 WAALAVGLLELWAAHALPAQVAFTYAPPGSTC--RLREYYDQTAQMCSCSPGQHAH 64
 DB 14 WGPLLLGLSLVA--SQPOLV--PPYRIE--NOTQDQDKEYEYEPHMDVHCVCKPGEFVF 69
 QY 65 VFCTKTSITVCDSCDSSTYTOLNWNVPECLSGSCSSDQV---ETOACTREQNRICTC 120
 DB 70 AVCSRSQDTVCKTCPHNSYNEHNLSTCOLCR---PCDIVLGFEVAVACTSDRAECRC 126
 QY 121 RPNWYCALSKQEGKRLCAPLRKRCRPGFVGVARPTET-----SDVVCPCAPGTFST 172
 DB 127 QPGMSCVYLDNE--CVHCEER-----LVLCQPGTEAEVTEIMDTDVCNCPKPGHFQNT 180
 QY 173 TSSDTICRPHQICN-----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLQPVPYSTRSQHTQ 228
 DB 181 SSPRACQPHTRCEIQGLVEAPGTSYSDTICKN----- 214
 QY 229 PTPEPSTAPSTFSLPMGPPSPAGSTGDFALPVGLVGTALGLLIIGVNVCMVIM--- 284
 DB 215 -PPEPGAMLLAILLSL-----VFLFLTTLVACANRRHPS 249
 QY 285 -----TOVKK-----KPLCLQREAKVPHLP-----ADKARGTQGPQQHLLIT 322
 DB 250 LCRKLGITLLKRPGEESPPCPAPRAD--PHFPDLAEPLLPMSGDLSPSPAGPP-----T 302
 QY 323 APSSSSSSLESASALDRARRTRNQPAQGVASGAGEARASTGSSDSSPGHGTVQNVNT 382
 DB 303 APSLEEVYLOQSSPLV-----QARELEAEFGEHQVAGAN-----GIHVTCGSVT 348
 QY 383 CIVNVCSSSHSSQCSQASSTMGDTSSPSKDEQVPE--SKEECAFRSQLETP 437
 DB 349 VTGNIYYIN-----GPVIGGT--RGPDPAPPPEPYPTPEGAPSELSTP 394
 RESULT 9
 TR14_HUMAN
 ID TR14_HUMAN STANDARD; PRT; 283 AA.
 AC Q92956; Q9UM65;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR
 DE (HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE 2)
 DE (TR2).
 GN TNFRSF14 OR HVEM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix adenocarcinoma;
 RX MEDLINE=97053782; PubMed=8898196;
 RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
 RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
 RL the TNF/NGF receptor family.";
 RL Cell 87:427-436(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97306336; PubMed=9162061;
 RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
 RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
 RA Porter T.G., Truneh A., Young P.R.;
 RT "A newly identified member of the tumor necrosis factor receptor
 RT superfamily with a wide tissue distribution and involvement in
 RT lymphocyte activation.";
 RL J. Biol. Chem. 272:14272-14276(1997).

RESULT 10	
CD40_MOUSE	
ID	CD40_MOUSE STANDARD; PRT; 289 AA.
AC	P27512;
DT	01-AUG-1992 (Rel. 23, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	CD40 RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN	TNFRSF5 OR CD40.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92105763; PubMed=1370315;
RA	Torres R.M., Clark E.A.;
RT	"Differential increase of an alternatively polyadenylated mRNA
RT	species of murine CD40 upon B lymphocyte activation.";
RN	J. Immunol. 148:620-626(1992).
RN	[2]
RP	REVISIONS.
RC	STRAIN=BALB/C;
RC	Torres R.M.;
RL	Submitted (SEP-1986) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C; TISSUE=Liver;
RX	MEDLINE=93094586; PubMed=1281194;
RA	Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA	Howard M., Cockayne D.A.;
RT	"Genomic structure and chromosomal mapping of the murine CD40 gene.";
RT	J. Immunol. 149:3921-3926(1992).
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M83312; AAB08705.1; -.
DR	EMBL; M94126; AAA37404.1; -.
DR	EMBL; M94129; AAA37404.1; JOINED.
DR	EMBL; M94128; AAA37404.1; JOINED.
DR	EMBL; M94127; AAA37404.1; JOINED.
DR	PIR; A6476; A46476.
DR	HSSP; P25942; ICDP.
DR	MGI; M8336; Tnf1sf5.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	ProDom; PD000771; TNFR_c6; 1.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS00500; TNFR_NGFR_2; 4.
KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT	SIGNAL 1 19 POTENTIAL.
FT	CHAIN 20 289
FT	DOMAIN 20 193
FT	TRANSMEM 194 215
FT	DOMAIN 216 289
FT	DOMAIN 25 187
FT	REPEAT 25 60
FT	REPEAT 61 103
FT	REPEAT 104 144
FT	REPEAT 145 187
FT	REPEAT 153 153
FT	CARBOHYD 289 AA; 32111 MW; C791CB6D2FEA574E CRG64;
SQ	SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRG64;

DR	PRODOM;	PD0007711; TNFR-C6; 1.	
DR	SMART;	PS00208; TNFR; 4.	
DR	PROSITE;	PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE;	PS00050; TNFR_NGFR_2; 4.	
KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.		
	SIGNAL	1 19	POTENTIAL.
FT	CHAIN	20 289	CD40L RECEPTOR.
FT	DOMAIN	20 193	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	194 215	POTENTIAL.
FT	DOMAIN	216 289	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	25 187	4 X TNFR-CYS.
FT	REPEAT	25 60	TNFR-CYS 1.
FT	REPEAT	61 103	TNFR-CYS 2.
FT	REPEAT	104 144	TNFR-CYS 3.
FT	REPEAT	145 187	TNFR-CYS 4.
FT	CARBOHYD	153 153	N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE	289 AA; 32111 MW; C791CBGD2FEA57AE CRG64;	

RESULT 12

```
CD40_BOVIN
ID CD40_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; U57745; AAC48710.1; -
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PSS0050; TNFR_NGFR_2; 1.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >269 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 9.8%; Score 242.5; DB 1; Length 269;
Best Local Similarity 31.0%; Pred. No. 8.1e-08;
Matches 63; Conservative 17; Mismatches 96; Indels 27; Gaps 6;

QY 23 LPAQVAF-----TPYAPPGSTCLREYYDQTQACMKSCSPGQHKVFTKTSVTCDSDS 77
DQ 4 LPLQLFWGFFLTAHVSEPATAACEKY--PVNSLCCDCLCPPGKLVNDCTEVSKTECSQ 61
QY 78 CEDSTYTLNWNWPEC-----LSCGRCSSDQVETQACTREONRITCTCRPGWYCALSK 130
DQ 62 CGGGEFLSTWNREKYCHHEHYCNPLRLIQSEG-----TLNTDTTCVCEVGHQCT--- 112
QY 131 QEGRLCAPLRKCRPGFVARPGTETSDVVKPCAPGTFSTNTSDTCRPHQTCN----- 186
DQ 113 SHTCESCTPHSLCLPGFVKQIATGLDVTCEPCPLGFFSNVSSAFKCHRWTSCKRGL 172
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QY 187 VVAIFGNASMDAVCTSTSTPSRSM 209
DQ 173 VEQHVGTNKTDDVVCVFQSRMRTL 195

RESULT 13
CD30_HUMAN
ID CD30_HUMAN STANDARD; PRT; 595 AA.
AC P28908;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN CD30) (KI-1
DE ANTIGEN).
GN TNFRSP8 OR CD30.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92154659; PubMed=1310894;
RA Duerkop H., Latza U., Hummel M., Eitelbach F., Seed B., Stein H.;
RT "Molecular cloning and expression of a new member of the nerve growth
RT factor receptor family that is characteristic for Hodgkin's
RT disease.";
RL Cell 68:421-427(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95089787; PubMed=7527901;
RA Jung W., Krueger S., Renner C., Gause A., Sahin U., Trumper L.,
RA Pfeundschtuh M.;
RT "Opposite effects of the CD30 ligand are not due to CD30 mutations:
RT results from cDNA cloning and sequence comparison of the CD30 antigen
RT from different sources.";
RL Mol. Immunol. 31:1329-1334(1994).
RN [3]
RP SEQUENCE FROM N.A. (VARIANT C30V).
RX MEDLINE=96437016; PubMed=8839832;
RA Horie R., Ito K., Tatewaki M., Nagai M., Aizawa S.,
RA Higashihara M., Ishida T., Inoue J., Takizawa H., Watanabe T.;
RT "A variant CD30 protein lacking extracellular and transmembrane domain
RT is induced in HL-60 by tetradecanoylphorbol acetate and is expressed
RT in alveolar macrophages.";
RL Blood 88:2422-2432(1996).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD30L. MAY PLAY
CC A ROLE IN THE REGULATION OF CELLULAR GROWTH AND TRANSFORMATION OF
CC ACTIVATED LYMPHOBLASTS. REGULATES GENE EXPRESSION THROUGH
CC ACTIVATION OF NFkB.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: A SHORTER CYTOPLASMIC FORM C30V WHICH IS
CC ONLY EXPRESSED IN ALVEOLAR MACROPHAGES IS PRODUCED BY THE USE
CC OF AN ALTERNATIVE INITIATION CODON IN THE SAME READING FRAME.
CC -!- PTM: PHOSPHORYLATED ON SERINE AND TYROSINE RESIDUES.
CC -!- DISEASE: MOST SPECIFIC HODGKIN'S DISEASE ASSOCIATED ANTIGEN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD30 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd30.htm".
CC -----
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CC -----
DR EMBL; M83554; AAA51947.1; -
DR EMBL; S75768; AAD14188.1; -
DR EMBL; D86042; BAA12973.1; -
DR PIR; A42086; A42086.
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DR HSP; P19438; INCF.
DR MIM; 153243; -.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
DR T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation; Alternative Initiation.
FT SIGNAL 1 18
FT CHAIN 19 595
FT CHAIN 464 595
FT INIT MET 464 464
FT DOMAIN 19 379
FT TRANSMEM 380 407
FT DOMAIN 408 595
FT DOMAIN 28 325
FT REPEAT 28 66
FT REPEAT 68 106
FT REPEAT 107 150
FT REPEAT 205 241
FT REPEAT 243 281
FT REPEAT 282 325
FT DOMAIN 347 377
FT CARBOHYD 101 101
FT CARBOHYD 276 276
SQ SEQUENCE 595 AA; 63747 MW; 7A407CC78A6E0BC8 CRC64;

Query Match
Best Local Similarity 22.0%; Pred. No. 2.1e-07; Length 595;
Matches 113; Conservative 41; Mismatches 183; Indels 176; Gaps 17;

QY 11 AVGLELWAAHALPAQVAFTPYAPEGSTC--RLRYYVDQTAQMCCKSPGQHAKEFT 68
DB 7 ALGLFLGALRAFPQDRPE-----DTCGNPNSHYDKAVRCCYRCPMGLFPTQOCP 59
QY 69 KTSDDTVCDSCEDSTYQLNWNVPECLSCGSCSSDDQVETQACTREONRICTRPGWYCAL 128
DB 60 QRPTDCRKOCEPDYLL---DEADRCTACVTCSSRDDLVKTPCAWNSRVRCECRPGMFCST 116
QY 129 SKOEGRLCAPLRCRPGFVGARPGTETSDVCKKCAPG----- 167
DB 117 SAVNSCARCFHSHVCPAGMIVKFPGTAQNTVCEPASPGVSPACASPENCKEPPSGTIPQ 176
QY 168 -----TFSNTT----- 173
DB 177 AKPTVPSPATSSASTVPRGGTRLAQEAASKLTPADSPSSVGRPSDDPGLSPTQCPGEG 236
QY 174 -----SSTDICRPHQICNVVAIPG 192
DB 237 SGDCRKOCEPDYLLDEAGRCTACVSCSRDDLVKTPCAWNSRRTCECRPGMICATSATNS 296
QY 193 NASMDAVCTSTSTRMARGAVHLPO-----PVSTRSQHTQTPPE-----PST 235
DB 297 -----CARCPVPYPTCAAEVTKPDMAEKDTTFEAPPLGTQPD-CNPTPENGAEPAST 348
QY 236 APSTSFEL-----LPMGPSP-ASGSTGDFALPGLVIGVATGALLIIGVNVCMVTMQ 286
DB 349 SPTQSLVDSQASKTLPIPTSAVALSSGKPVLDAGPVLFVWILVLVVVGSSAFLLCH 408
QY 287 VKKKPLCLQREAKVPHL--PADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPT 344
DB 409 ---RRACRKRIKRLHLCYVPQ---TSQPKLE-LVDSRRPRSSSTQLRSGASVTEPVAEE 460
QY 345 R---NQPAQGVASGAGERASTGSSDSPG 374
DB 461 RGLMSQPLMETCHSVGAAYLE-SLPLQDASPAG 492

RESULT 14
OX40_RAT
ID OX40_RAT STANDARD; PRT; 271 AA.
```

```
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=T-cell;
RC MEDLINE=90214614; PubMed=2157591.
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RT lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBO J. 9:1063-1068(1990).
CC -|- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -|- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -|- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DR EMBL; X17037; CAA34897.1; .
DR PIR; S08036; S08036.
DR PIR; S12783; S12783.
DR HSP; P25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRODOM; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 271
FT DOMAIN 20 210
FT TRANSMEM 211 235
FT DOMAIN 236 271
FT DOMAIN 25 164
FT REPEAT 25 60
FT REPEAT 61 102
FT REPEAT 103 123
FT REPEAT 124 164
FT CARBOHYD 143 143
FT SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match
Best Local Similarity 9.3%; Score 229.5; DB 1; Length 271;
Matches 79; Conservative 28; Mismatches 88; Indels 97; Gaps 14;

QY 6 VW-----AALAVGLELWAAHALPAQVAFTPYAPEGSTGRLREYD--QTAQMCCSKS 58
DB 3 VVWQPTAFLLGLSL-----GVTVKLNCVKDYTPSGHKCCRECQ 42
QY 59 PGQHAKEFTKTSVTQSCDSTYQLNWN--VPECLSCGSCSSDDQVETQACTREQNR 116
DB 43 PGHGMVSRCDTRDTVCHPCPEPGFYNEAVNYDKQCTQCNRHSGSEL--KQNCPTPTDT 100
QY 117 ICTCRPGHYCALSKQEGCRCLCAPLRCRPGFVGARPGTETS---DVVCKPCAPGTFSTNT 173
DB 101 VCOCRPG-----TOPRODSSHKLGVDCVPCPGHFS---P 132
```

```
QY 174 SSTICRPHQICNV-----VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT-- 227
Db 133 GSNACKPWTNCTLSGKQIRHPASNSLDTVCEDRS-----LLATLLWETQRTTF 181
QY 228 OPTPEPSTA-----PSTGDFAL-PMGSPSPAEGSTGDFALPVGLIVGVTA 270
Db 182 RPTTVPTVTPWPTSQLPSTPTTLVAPEGPA-----FAVILGLGLGLLA 224

RESULT 15
OX40_MOUSE
ID OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions."
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.B., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein."
RL Eur. J. Immunol. 25:926-930(1995).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC -----
DR EMBL; Z21674; CAA79772.1; -
DR EMBL; X85214; CAA59476.1; -
DR HSP; P25942; ICDP.
DR MGD; MGI:104512; Tnfrsf4.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 272 OX40L RECEPTOR.
FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 212 236 POTENTIAL.
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
```

```
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 9.1%; Score 223.5; DB 1; Length 272;
Best Local Similarity 27.0%; Pred. No. le-06;
Matches 88; Conservative 32; Mismatches 97; Indels 109; Gaps 19;

QY 6 VW-----AALAVGLELWAAHALPAQVAFTPYAPEGSTCRRLREYVDQTAQMCCSKCSPG 60
Db 3 VWQOFTALLLLALTGLVTARRL-----NCVKHTY--PSGHKCCRECQPG 45
QY 61 QHAKVCTKTSIDTVCDCSDSTVTQLWNW--VPECLSCGSRCSDDQVETQACTREQNRIC 118
Db 46 HGMVSRCDHTRDTLCHPCETGFEYNEAVNYDTCKQCTQCNRHSGSEL--KQNCITPTQDTCV 103
QY 119 TCRPGWYCALSKOEGCRCLCAPLRKCRPGFVARPGTETS---DVCKKPCAPGTFSTNTSS 175
Db 104 RCRPG-----TQPRQDSGVKLGVDVCPGPPGHFS--PGN 135
QY 176 TDCRPHQICNV-----VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQ-PT 230
Db 136 NOACKPWTNCTLSGKQTRHPASDSLDVAVCED-----RSL-----LATLLWETQRT 181
QY 231 PEPSTA-----PSTSFLLPMGPPSPA-----EGSTGDFALPVGLIVGVTA-LGLLIIGVV 279
Db 182 FRPTTVQSTTVWPTSEL-----PSPPTLVTPGPA--FAVILGLGLGLLAPLVLL----- 231
QY 280 NCVIMTQVKKKPLCLQREA-KVPHLP 304
Db 232 -----ALYLLLRKAWRLPNT 246

Search completed: February 12, 2002, 12:51:31
Job time: 207 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:47:13 ; Search time 28.69 Seconds
(without alignments)
2350.350 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEKPLPLGVDPAGMKRPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2279	92.3	425	4 Q16042	Q16042 homo sapien
2	1498	60.7	482	11 O88734	O88734 mus musculus
3	1477	59.8	459	11 O62327	O62327 mus musculus
4	826	33.5	161	4 Q9UJQ3	Q9UJQ3 homo sapien
5	503.5	20.4	175	11 Q9WUL4	Q9WUL4 rattus norv
6	482	19.5	92	4 Q9UIG9	Q9UIG9 homo sapien
7	409	16.6	78	4 Q9UIH0	Q9UIH0 homo sapien
8	390.5	15.8	349	12 O57101	O57101 monkeypox v
9	389.5	15.8	349	12 O57291	O57291 monkeypox v
10	389.5	15.8	349	12 O57102	O57102 monkeypox v
11	389	15.8	348	12 O57277	O57277 monkeypox v
12	389	15.8	348	12 O57103	O57103 monkeypox v
13	389	15.8	348	12 O57108	O57108 monkeypox v
14	386.5	15.7	349	12 O57099	O57099 monkeypox v
15	385	15.6	349	12 O57284	O57284 camelpox vi
16	385	15.6	349	12 O57098	O57098 camelpox vi
17	383.5	15.5	349	12 O57100	O57100 monkeypox v
18	381.5	15.5	349	12 O57111	O57111 variola vir
19	381.5	15.5	349	12 Q89098	Q89098 variola vir

20	381	15.4	347	12	O57115	O57115 cowpox viru
21	381	15.4	349	12	O57097	O57097 camelpox v1
22	379.5	15.4	348	12	O57112	O57112 variola vir
23	379.5	15.4	348	12	O85407	O85407 variola vir
24	378	15.3	347	12	O57119	O57119 cowpox viru
25	377	15.3	360	12	O57118	O57118 cowpox viru
26	376.5	15.3	349	12	O57110	O57110 variola vir
27	376.5	15.3	349	12	O89118	O89118 variola vir
28	374	15.2	351	12	O57117	O57117 cowpox viru
29	374	15.2	351	12	O57121	O57121 cowpox viru
30	373	15.1	351	12	O73559	O73559 cowpox viru
31	373	15.1	355	12	O85308	O85308 cowpox viru
32	371.5	15.1	349	12	O57109	O57109 variola vir
33	370.5	15.0	350	12	O57116	O57116 cowpox viru
34	368	14.9	349	12	O57305	O57305 cowpox viru
35	359	14.5	350	12	O57123	O57123 cowpox viru
36	354.5	14.4	326	12	O57122	O57122 cowpox viru
37	351.5	14.2	300	4	O95407	O95407 homo sapien
38	345.5	14.0	326	12	O57120	O57120 cowpox viru
39	343.5	13.9	655	4	O75509	O75509 homo sapien
40	339	13.7	316	12	O57092	O57092 ectromelia
41	339	13.7	320	12	O57091	O57091 ectromelia
42	339	13.7	320	12	O57300	O57300 ectromelia
43	330	13.4	320	12	O57079	O57079 cowpox viru
44	330	13.4	322	12	O72761	O72761 cowpox viru
45	330	13.4	372	4	Q9UHP4	Q9UHP4 homo sapien

ALIGNMENTS

RESULT 1

Q16042	ID	Q16042	PRELIMINARY;	PRT;	425 AA.
AC	Q16042;				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91370690; PubMed=1966549;				
RA	Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,				
RA	Brockhaus M., Lesslauer W.;				
RT	"Two human TNF receptors have similar extracellular, but distinct				
RL	intracellular, domain sequences.";				
DR	Cytokine 2:231-237(1990).				
DR	EMBL; S63368; AAB19824.2; -.				
DR	HSSP; P25942; ICDF				
DR	InterPro; IPR001368; TNFR_c6.				
DR	Pfam; PF00020; TNFR_c6; 4.				
DR	ProDom; PD000771; TNFR_c6; 1.				
DR	SMART; SM00208; TNFR; 4.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.				
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.				
KW	Receptor.				
FT	NON_TER				
SQ	SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;				

Query Match		92.3%;	Score 2279;	DB 4;	Length 425;
Best Local Similarity		100.0%;	Pred. No. 4.4e-168;		
Matches 425;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	37	GSTCKRLREYYDQTQACMCCSKCSPGOHAKVFCVTKTSDTVCDSCEDSDTYTQLWNVPCCLSC	96		
Db	1	GSTCKRLREYYDQTQACMCCSKCSPGOHAKVFCVTKTSDTVCDSCEDSDTYTQLWNVPCCLSC	60		
Qy	97	GSRCSSDQVETQACTREQNRICTRCPGNYCALSKQEGCRLCAPLRKRCRPGFGVARGTGT	156		

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Db 61 GSRSSDQVETQACTREQNRICTCPGNYCALSKOEGCRLCAPLRKCRPGFVARPGTET 120
Qy 157 SDVYCKPCAPGTFSTNTSDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPCAVHL 216
Db 121 SDVYCKPCAPGTFSTNTSDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPCAVHL 180
Qy 217 PQPVSTRSQHTQPTPEPSTAFSTFLLPMGPSPPAEGSTGDFALPVGLVGTALGLLII 276
Db 181 PQPVSTRSQHTQPTPEPSTAFSTFLLPMGPSPPAEGSTGDFALPVGLVGTALGLLII 240
Qy 277 GVNVCVIMTQVKKPKLQREAKVPHLPADKARGTQGGPEQOHLITAPSSSSSSLESSAS 336
Db 241 GVNVCVIMTQVKKPKLQREAKVPHLPADKARGTQGGPEQOHLITAPSSSSSSLESSAS 300
Qy 337 ALDRAPTRNPOAPGVCASGAGEARASTGSSDSPGGHGTVQNVNVCIVNVCSDDHSSQ 396
Db 301 ALDRAPTRNPOAPGVCASGAGEARASTGSSDSPGGHGTVQNVNVCIVNVCSDDHSSQ 360
Qy 397 CSSQASSTMGTDSSPSPKDEQVPFKECAFRSQLETPETLLGSTEEKPLPLGVDPDA 456
Db 361 CSSQASSTMGTDSSPSPKDEQVPFKECAFRSQLETPETLLGSTEEKPLPLGVDPDA 420
Qy 457 GSKPS 461
Db 421 GSKPS 425

RESULT 2
O88734 PRELIMINARY; PRT; 482 AA.
AC O88734
DT 01-NOV-1998 (TremBLrel. 08, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and
RT Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).
DR EMBL; Y14619; CAA74969.1; JOINED.
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;
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Query Match 60.78; Score 1498; DB 11; Length 482;
Best Local Similarity 62.88; Pred. No. 8e-108;
Matches 297; Conservative 49; Mismatches 111; Indels 16; Gaps 9;

Qy 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCP 59
Db 1 MAPAALWVALVFELQWLWAGTIVPAQVVLTPYKPEPGYECQLSQEYIDRKAKMCCAKCP 60
Qy 60 GQHAKVFCTKTSDTV-DS-----CEDSTYTQLWNWVPECLSCGSRGSSDQVETQACTR 112
||:~|| || ||||| || || ||||| || || ||||| || || ||||| ||||| ||||| |||||
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Db 61 GOYVHKFNKTSDTVCAADSDTVCAACEASMYTQVWNOFRTCLSCSSSCSDQVETRACTK 120
Qy 113 EQNRICTRPGWYCALSKOEG-CRLCAPLRKCRPGFVARPGTETSDVYCKPCAPGTFSN 171
Db 121 QNRVACAEAGRYCALKTHSGSCRCMRLSKCGPGFVASSRAPNGNVLCACAPGTFSD 180
Qy 172 TTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPT 231
Db 181 TTSSTDVCRPHRICSLAIPGNASTDAVCAPESPTLSAIPRTLVSQPEPTRSQPLDQEP 240
Qy 232 EPSTAPSTFLLPMGPSPPAEGST-GDFALPVGLIVGTALGLLIIIGVNVCVIMTQVKKK 290
Db 241 GPSQTP--SILTSLSGSTPIEQSTKGISLPIGLIVGTSLGLMLGLVNCFLVORKKK 298
Qy 291 PCLQREAKVPHLPADKARGTQGGPEQOHLITAP-SSSSSSLESSASALDRRAPTRNPOQ 349
Db 299 PCLQREAKVPHVPDEKSQDAVLEQOHLITAPSSSSSSLESSASAGDRRAPPGGHQ 358
Qy 350 APGV-EASGAGBARASTGSSDSPGGHGTVQNVNVCIVNVCSDDHSSQSSQASSTMGDT 408
Db 359 ARVMAEAOQSQEARASSRISDSHSGHGHVNVNVCIVNVCSDDHSSQSSQASATVGD 418
Qy 409 DSSPSPKDEQVPFKECAFRSQLETPETLLGSTEEKPLPLGVDPDAGMKPS 461
Db 419 DAKPSAPKDEQVPFQEECPSPQPYETETL--QSHEKPLPLGVDPDGMKPS 469

RESULT 3
Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
FT NON_TER 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;
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Query Match 59.88; Score 1477; DB 11; Length 459;
Best Local Similarity 63.88; Pred. No. 3.2e-106;
Matches 287; Conservative 47; Mismatches 108; Indels 8; Gaps 6;

Qy 16 LWAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCPQHAKVFCTKTSDTV 74
||| | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 LWATGTVPAQVVLTPYKPEPGYECQLSQEYIDRKAKMCCAKCPGQYVKKHFNKTSDTV 60
Qy 75 CDSCEDSTYTQLWNWVPECLSCGSRGSSDQVETQACTREQNRICTCRPGWYCALSKOEG - 133
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Db 61 CADCEASMTQVWVNFRTCLSCSSCSTDOVETRACTKQNRVYACAGRYCALKTHSGS 120
QY 134 CRICAPLRCRPGFGVARGTETSDVVCKPCAGTSTNTSDICRPHQICNVVAIPGN 193
Db 121 CROCMLRSCGPGFGVASSRAPNGVNLCKACAPGTSDTSTSDVCRPHRICSLAIPGN 180
QY 194 ASMDAVCTSTSPTRSMAGVAVHLPQVSTRSOHTQTPPEPSTAPSTSFLLPMGSPSAPG 253
Db 181 ASDVAVCAPESPTLSAIPRTLVYSQPEPTRSQPLDQEGPSQTP--SILTSLGSTPIEQ 238
QY 254 ST-GDPALPVGLIVGTALGLLIIGVNVCMVTOVKKKPLCLQREAKVPHLPADKARGTQ 312
Db 239 STKGGISLIGLIVGTSGLLMLGVNCFILVQRKKKPSCLORDAKVPHVPEKSDAV 298
QY 313 GPEQOHLITAPSSSSSSLESSASALDRAPTRNQPAQGV-EASGAGEARASTGSSDSS 371
Db 299 GLEQOHLITAPSSSSSSLESSASAGDRRAPPGGHPQARYMAEAQGSQEARASSRISDSS 358
QY 372 PGHGTQVNVTCIVNVCCSSDSSSQSSQASSTMGTDSSPSPKDEQVFPFSKECAFR 431
Db 359 HGSHTVNVTCIVNVCCSSDSSSQSSQASATVGDPAKPSAPKDEQVFPFSKECPQ 418
QY 432 SOLETETLLGSTEEKPLPLGVDPAGMKPS 461
Db 419 SPYETTEL--QSHKPLPLGVDPAGMKPS 446

RESULT 4
Q9UJ03 ID Q9UJ03 PRELIMINARY; PRT; 161 AA.
AC Q9UJ03
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE DJ111824.3 (TUMOR NECROSIS FACTOR RECEPTOR 2 (75 KDA) (TNF BINDING
PROTEIN 2, TBPII, TNF-R2, CD120B, TNFR)) (FRAGMENT).
GN TNFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031276; CAA20343.1; -.
FT NON_TER 1
SQ SEQUENCE 161 AA; 16449 MW; E6C96E774B5CF7B0 CRC64;

Query Match 33.5%; Score 826; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 PHLPADKARGTQGPQOHLITAPSSSSLESSASALDRAPTRNQPAQGVASGAGE 360
Db 1 PHLPADKARGTQGPQOHLITAPSSSSLESSASALDRAPTRNQPAQGVASGAGE 60
QY 361 ARASTGSSDSSPGHGTQVNVTCIVNVCCSSDSSSQSSQASSTMGTDSSPSPKDEQ 420
Db 61 ARASTGSSDSSPGHGTQVNVTCIVNVCCSSDSSSQSSQASSTMGTDSSPSPKDEQ 120
QY 421 VPFSKECAFRSOLETPETLLGSTEEKPLPLGVDPAGMKPS 461
Db 121 VPFSKECAFRSOLETPETLLGSTEEKPLPLGVDPAGMKPS 161

RESULT 5
Q9WU04 ID Q9WU04 PRELIMINARY; PRT; 175 AA.
AC Q9WU04
DT 01-NOV-1999 (TReMBLrel. 12, Created)
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DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=OVARY;
RA Balchak S.K., Marcinkiewicz J.L.;
RT "Evidence for the Presence of Tumor Necrosis Factor Alpha Receptors
During Ovarian Development in the Rat.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF142499; AAD30148.1; -.
DR InterPro; IPR001368; TNFR_C6.
DR SMART; SM00208; TNFR; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 175
SQ SEQUENCE 175 AA; 18201 MW; 499EADAAB21ED8B CRC64;

Query Match 20.4%; Score 503.5; DB 11; Length 175;
Best Local Similarity 55.9%; Pred. No. 1.4e-31;
Matches 99; Conservative 23; Mismatches 52; Indels 3; Gaps 2;

QY 147 FGVARPGTETSDVVCKPCAGTSTNTSDICRPHQICNVVAIPGNASMDAVCTSTPT 206
Db 1 FGVASRTSNGNVICSACAPGTFSDTSTSDVCRPHRICSLAIPGNASTDAVCASEPT 60
QY 207 RSMAPGAVHLPQVSTRSQHTQTPPEPSTAPSTSFLLPMGSPSPAEGS-TGDFALPVGLI 265
Db 61 PSAGPTIIVSQPEPTRSQPMGQEPGSPQTPHIP--VSLGSTPIIEPSITGGISLPIGLI 118
QY 266 VGV TALGLLIIGVNVCMVTOVKKKPLCLQREAKVPHLPADKARGTQGPQOHLIT 322
Db 119 VGLTTLGLMLGLATCFILVQRKKKPSCLQRETMVPHLPDDKSDQAIGLEQOHLIT 175

RESULT 6
Q9UIG9 ID Q9UIG9 PRELIMINARY; PRT; 92 AA.
AC Q9UIG9
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
GN TNFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Komata T., Tsuchiya N., Matsushita M., Tokunaga K.;
RT "New polymorphism within the extracellular region of TNFR2.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030952; BAA89055.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 92 AA; 9530 MW; 89BDE40B7CC4FE1 CRC64;

Query Match 19.5%; Score 482; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 SSPGCHGTQVNVTCIVNVCCSSDSSSQSSQASSTMGTDSSPSPKDEQVFPFSKECA 429
Db 1 SSPGCHGTQVNVTCIVNVCCSSDSSSQSSQASSTMGTDSSPSPKDEQVFPFSKECA 60
QY 430 FRSOLETPETLLGSTEEKPLPLGVDPAGMKPS 461
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Db 61 FRSOLETPETLLGSTEKPLPLGVDPAGMKPS 92

RESULT 7
Q9UIH0
ID Q9UIH0 PRELIMINARY; PRT; 78 AA.
AC Q9UIH0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
GN TNFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Komata T., Tsuchiya N., Matsushita M., Tokunaga K.;
RT "New polymorphism within the extracellular region of TNFR2.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB030951; BAA89054.1; -.
KW Receptor.
FT NON_TER 1 1
FT VARIANT 48 48 K -> E.
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 7841 MW; 3A219A37EAPE0719 CRC64;

Query Match 16.6%; Score 409; DB 4; Length 78;
Best Local Similarity 98.7%; Pred. No. 1.3e-24;
Matches 77; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 185 CNVVAIPGNASMDAVCTSTSTRMAPCAVHLPOVSTRSHTOPTPEPSTAPSTSLFP 244
Db 1 CNVVAIPGNASMDAVCTSTSTRMAPCAVHLPOVSTRSHTOPTPEPSTAPSTSLFP 60
QY 245 MGPSPPAEGSGTGDFALPV 262
Db 61 MGPSPPAEGSGTGDFALPV 78

RESULT 8
ID Q57101 PRELIMINARY; PRT; 349 AA.
AC Q57101
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1377 (77-0666);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U87845; AAB94362.1; -.
DR HSSP: P25942; 1CDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38311 MW; 02F65B00CFB58BE CRC64;

Query Match 15.8%; Score 390.5; DB 12; Length 349;

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Best Local Similarity 41.8%; Pred. No. 1.4e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

QY 31 PYAPEPGSTCLRREYDQTAQMCCKSPGQHAKEVCTKTSTVDCSDCEDSTYTLWNV 90
Db 24 PHAPSNKG-CKDNEY--RSRLCCLSCPPGTYSRLCDSKTNTQCTPCGSDFTSHNNHL 80
QY 91 PECLSCGSRCSDDQVETQACTREQNRICTRCPGWYCALSKQEGCRCLCAPLRKCRPGFGVA 150
Db 81 QACLSCNGRCDSNQVETRSCNTTHNRICECPGYVCLLKGSSGCRCTCISKTKGIGYGV 140
QY 151 RPTGTSVWCKPCAPGTFSNTTSTSDICRPHQICN-----VVAIPGNASMDAVCTS 202
Db 141 -GYTSTGDIVCSPCGPGTYSHTVSTSDKCEPVVTSNTFNIDVEINLYPVN----DTSC 196
QY 203 TSPT 206
Db 197 TTTT 200

RESULT 9
Q57291
ID Q57291 PRELIMINARY; PRT; 349 AA.
AC Q57291
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U88144; AAB94369.1; -.
DR EMBL: U87842; AAB94359.1; -.
DR EMBL: U87994; AAB94365.1; -.
DR EMBL: U87995; AAB94366.1; -.
DR EMBL: U88143; AAB94368.1; -.
DR HSSP: P25942; 1CDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38295 MW; CBD2C949ED2B8E7C CRC64;

Query Match 15.8%; Score 389.5; DB 12; Length 349;
Best Local Similarity 41.8%; Pred. No. 1.7e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

QY 31 PYAPEPGSTCLRREYDQTAQMCCKSPGQHAKEVCTKTSTVDCSDCEDSTYTLWNV 90
Db 24 PHAPSNKG-CKDNEY--RSRLCCLSCPPGTYSRLCDSKTNTQCTPCGSDFTSHNNHL 80
QY 91 PECLSCGSRCSDDQVETQACTREQNRICTRCPGWYCALSKQEGCRCLCAPLRKCRPGFGVA 150
Db 81 QACLSCNGRCDSNQVETRSCNTTHNRICECPGYVCLLKGSSGCRCTCISKTKGIGYGV 140
QY 151 RPTGTSVWCKPCAPGTFSNTTSTSDICRPHQICN-----VVAIPGNASMDAVCTS 202
Db 141 -GYTSTGDIVCSPCGPGTYSHTVSTSDKCEPVVTSNTFNIDVEINLYPVN----DTSC 196
QY 203 TSPT 206
Db 197 TTTT 200

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RESULT 10
O57102 PRELIMINARY; PRT; 349 AA.
AC O57102;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BENIN-1978 (78-3945);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match 15.8%; Score 389.5; DB 12; Length 349;
Best Local Similarity 41.8%; Pred. No. 1.7e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

QY 31 PYAPEPGSTCRLEYDQTAQMCCSKCPGQHAKEVCTKTSTVDCSDCEDSTYTQLWNWV 90
DB 24 PHAPSNKG-KADNEY--RSRLNCLCLSCPPGYASRLCDSKNTQTCTCGSDTFTSHNHL 80
QY 91 PECLSCGRSSDQVETQACTREQNRICTRPGWYCALSKQEGCRICAPLRKCRPGFGVA 150
DB 81 QACLSCNGRCDNQVETRSCNTHNRICECPGYVYLLKGGSGCRTCTCKTCGIGYGV 140
QY 151 RPTGTSDDVCKPCAPGTFSNTSTDCRPHQICN-----VVAIPGNASMDAVCTS 202
DB 141 -GYTSTGDVICSPGPGTYSHVTSSTDKCEPVVTSNTFNYIDVEINLYPNV---DTSCTR 196
QY 203 TSP 206
DB 197 TTTT 200

RESULT 11
O57277 PRELIMINARY; PRT; 348 AA.
AC O57277;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87841; AAB94358.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
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DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

Query Match 15.8%; Score 389; DB 12; Length 348;
Best Local Similarity 42.1%; Pred. No. 1.8e-22;
Matches 77; Conservative 22; Mismatches 70; Indels 14; Gaps 6;

QY 31 PYAPEPGSTCRLEYDQTAQMCCSKCPGQHAKEVCTKTSTVDCSDCEDSTYTQLWNWV 90
DB 24 PHAPSNKG-KADNEY--RSRLNCLCLSCPPGYASRLCDSKNTQTCTCGSDTFTSHNHL 80
QY 91 PECLSCGRSSDQVETQACTREQNRICTRPGWYCALSKQEGCRICAPLRKCRPGFGVA 150
DB 81 QACLSCNGRCDNQVETRSCNTHNRICECPGYVYLLKGGSGCRTCTCKTCGIGYGV 140
QY 151 RPTGTSDDVCKPCAPGTFSNTSTDCRPHQICN-----VVAIPGNASMDAVCTS 202
DB 141 -GYTSTGDVICSPGPGTYSHVTSSTDKCEPVVTSNTFNYIDVEINLYPNV---DTSCTR 196
QY 204 SPT 206
DB 197 TTT 199

RESULT 12
O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1979 (79-0005);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB94364.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 15.8%; Score 389; DB 12; Length 348;
Best Local Similarity 42.1%; Pred. No. 1.8e-22;
Matches 77; Conservative 22; Mismatches 70; Indels 14; Gaps 6;

QY 31 PYAPEPGSTCRLEYDQTAQMCCSKCPGQHAKEVCTKTSTVDCSDCEDSTYTQLWNWV 90
DB 24 PHAPSNKG-KADNEY--RSRLNCLCLSCPPGYASRLCDSKNTQTCTCGSDTFTSHNHL 80
QY 91 PECLSCGRSSDQVETQACTREQNRICTRPGWYCALSKQEGCRICAPLRKCRPGFGVA 150
DB 81 QACLSCNGRCDNQVETRSCNTHNRICECPGYVYLLKGGSGCRTCTCKTCGIGYGV 140
QY 151 RPTGTSDDVCKPCAPGTFSNTSTDCRPHQICN-----VVAIPGNASMDAVCTS 202
DB 141 -GYTSTGDVICSPGPGTYSHVTSSTDKCEPVVTSNTFNYIDVEINLYPNV---DTSCTR 196
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Qy 204 SPT 206
Db 197 TTT 199

RESULT 13
O57108
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 15.8%; Score 389; DB 12; Length 348;
Best Local Similarity 42.1%; Pred. No. 1.8e-22;
Matches 77; Conservative 22; Mismatches 70; Indels 14; Gaps 6;

Qy 31 PYAPEGSTCLREYYDQTAQMCCSKCSPGOHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
Db 24 PHAPSNKG-CKDNEY--RSRNLCCLSPPGTYASRLCDKNTQCTPCGSDTFTSHNNHL 80
[1]
Qy 91 PECLSCGRSSDQVETQACTREONRICTCRPGWYCALSKQEGCRCLAPLRKCRPGFGVA 150
[1]
Db 81 QACLSCNGRCDNQVETRSCNTHNRICECSPGYCYLLKGSGGCTCLSKTKCGIGYGV 140
[1]
Qy 151 RPTGTSVVCPCAPGTFSTSTSDICRP--HQICNVAI-----PGNASMDAVCTST 203
Db 141 -GYTSTGDIVCSPGPGTYSHVSTSDKCEPVTNTFNVIDEINLYPVN---DTSCRT 196
[1]
Qy 204 SPT 206
Db 197 TTT 199

RESULT 14
O57099
ID O57099 PRELIMINARY; PRT; 349 AA.
AC O57099;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIERRA LEONE-1970 (70-0266);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
```

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RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87843; AAB94360.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38321 MW; FE449028CC933F57 CRC64;

Query Match 15.7%; Score 386.5; DB 12; Length 349;
Best Local Similarity 41.8%; Pred. No. 2.8e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

Qy 31 PYAPEGSTCLREYYDQTAQMCCSKCSPGOHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
Db 24 PHAPSNKG-CKDNEY--RSRNLCCLSPPGTYASRLCDKNTQCTPCGSDTFTSHNNHL 80
[1]
Qy 91 PECLSCGRSSDQVETQACTREONRICTCRPGWYCALSKQEGCRCLAPLRKCRPGFGVA 150
[1]
Db 81 QACLSCNGRCDNQVETRSCNTHNRICECSPGYCYLLKGALGCRCTCISKTKGIGYGV 140
[1]
Qy 151 RPTGTSVVCPCAPGTFSTSTSDICRP--HQICNVAI-----VVAIFGNASMDAVCTS 202
Db 141 -GYTSTGDIVCSPGPGTYSHVSTSDKCEPVTNTFNVIDEINLYPVN---DTSCRT 196
[1]
Qy 203 TSPT 206
Db 197 TTTT 200

RESULT 15
O57284
ID O57284 PRELIMINARY; PRT; 349 AA.
AC O57284;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Camelopox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=28873;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DUBAI-1992 (CP-5), SOMALIA-1978;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87840; AAB94357.1; -.
DR EMBL; U87837; AAB94354.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38036 MW; EA412AE86E090E4 CRC64;

Query Match 15.6%; Score 385; DB 12; Length 349;
Best Local Similarity 39.7%; Pred. No. 3.7e-22;
Matches 75; Conservative 19; Mismatches 71; Indels 24; Gaps 5;

Qy 30 TPYAPEPGSTCLREYYDQTAQMCCSKCSPGOHAKVFCTKTSDTVCDSCEDSTYTQLWNW 89
Db 23 TPYAPSNKG-CKDNEY--KRNLCCLSPPGTYASRLCDKNTQCTPCGSGTFTSRNNH 79
[1]
Qy 90 VPECLSCGRSSDQVETQACTREONRICTCRPGWYCALSKQEGCRCLAPLRKCRPGFGV 149
[1]
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Db 80 lPACLSGRCDSNQVETRSCNTHNRICECPGYICILKGSGCKACVSOQKCGIGYV 139.
QY 150 ARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA-----SMD 197
Db 140 S-GHTSAGDVICSPCGLGTYSRTVSSADKCEP-----VPSNTFNYIDVEINLYPVND 190
QY 198 AVCTSTSTPT 206
Db 191 TSCTRTTTT 199

Search completed: February 12, 2002, 12:50:47
Job time: 214 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:44:58 ; Search time 24.82 Seconds
(without alignments)
1375.817 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLCVDPAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT.*
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21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468	100.0	461	12	AA191141 Human TNF-R deduce
2	2468	100.0	461	14	AA192058 Fibroblast derived
3	2468	100.0	461	21	AA19717 A human tumour nec
4	2462	99.8	461	12	AA191001 40KD TNF inhibitor
5	2462	99.8	461	21	AA197801 Human tumour necro
6	2462	99.8	461	21	AA191342 Death receptor. H
7	2462	99.8	461	22	AA195331 Human TNF receptor
8	2462	99.8	461	22	AA196698 Human tumour necro
9	2462	99.8	461	22	AA197686 Human 40 kDa TNF i
10	2394	97.0	461	16	AA197504 p75 Tumour Necrosi
11	2376	96.3	461	15	AA1951002 Sequence of human

	12	2051.5	83.1	392	20	AA193935	Human tumour necro
	13	2050.5	83.1	392	12	AA191605	Human 75KD TNF-bin
	14	1506	61.0	474	12	AA191142	TNF-R deduced from
	15	1433	58.1	518	22	AA1970001	STNFR(075):Fc fusi
	16	1433	58.1	518	22	AA195080	TNFR:Fc fusion pro
	17	1424	57.7	518	15	AA1951003	Sequence of a reco
	18	1404	56.9	485	13	AA1924016	Fusion protein TNF
	19	1381	56.0	248	21	AA194718	Human type 2 tumou
	20	1318	53.4	235	21	AA194443	Wild type N-termina
	21	1315	53.3	235	21	AA194440	Amino acid sequenc
	22	1315	53.3	235	21	AA194441	Amino acid sequenc
	23	1312	53.2	235	19	AA195665	Human soluble tumo
	24	1312	53.2	235	19	AA1952270	Tumour necrosis fa
	25	1312	53.2	235	20	AA1989234	Tumour necrosis in
	26	1312	53.2	235	21	AA194442	A K108R/K120R muta
	27	1312	53.2	235	22	AA1937685	Human 40 kDa TNF 1
	28	1263	51.2	227	22	AA1966981	Tnfr2 protein. Un
	29	1256	50.9	225	21	AA197463	Primate protein se
	30	1116	45.2	198	21	AA194720	Human type 2 tumou
	31	1028	41.7	183	16	AA1977421	BamTP delta53 nerv
	32	937	38.0	165	21	AA1900014	Peptide fragment o
	33	935	37.9	163	21	AA194712	Tumour necrosis fa
	34	856	34.7	159	22	AA1937683	Human 40 kDa TNF 1
	35	794.5	32.2	258	22	AA1950082	Rat TNFR (p80) ext
	36	794.5	32.2	487	22	AA1950084	TNFR:Fc fusion pro
	37	770	31.2	227	21	AA1977462	Rodent protein seq
	38	707	28.6	122	19	AA1952271	Truncated soluble
	39	695	28.2	120	22	AA1966991	Human TNF-II pepti
	40	551	22.3	93	22	AA1937684	Human 40 kDa TNF 1
	41	477	19.3	802	16	AA1970111	TBP11-GBP 130 fusi
	42	470	19.0	802	16	AA1970112	TNF-R-GBP 130 fusi
	43	453	18.4	77	20	AA194641	TNF-R extracellular
	44	453	18.4	77	22	AA1969193	Human TNF-R extrac
	45	379.5	15.4	349	22	AA1950523	Human tumour necro

ALIGNMENTS

RESULT 1
AA191141
ID AA191141 standard; Protein; 461 AA.
XX
AC AA191141;
XX
24-MAY-1991 (first entry)
XX
Human TNF-R deduced from clone 1.
XX
Tumour necrosis factor receptor; Immune response; inflammation;
KW cachexia; septic shock.
XX
Homo sapiens.
XX
Key Location/Qualifiers
FH Peptide 1..22
FT /label= signal sequence
FT Protein 23..461
FT /label= TNF receptor
FT Domain 258..287
FT /label= transmembrane region
XX
EP418014-A.
XX
20-MAR-1991.
XX
10-SEP-1990; 90EP-0309875.
XX
10-MAY-1990; 90US-0523635.
XX
11-SEP-1989; 89US-0405370.
XX
13-OCT-1989; 89US-0421417.
XX
(IMMU-) IMMUNEX CORP.
PA

XX Smith CA, Goodwin RG, Beckmann PM;
 XX WPI: 1991-082230/12.
 DR N-PSDB; AAQ10990.
 XX
 PT New tumour necrosis factor -alpha and -beta receptors - and DNA
 PT encoding these used to regulate immune responses in treatment of
 PT cachexia, septic shock or side-effects of cytokine therapy.
 XX
 PS Disclosure; Fig 2; 41pp; English.
 XX
 CC The sequence was deduced from a DNA sequence obtd. from a clone
 CC isolated from a library prepd. from a human fibroblast cell line,
 CC WT-26 V44 (ATCC CCL 95.1). The clone is deposited as Accession No.
 CC 68088 under the name pCAV/NOT-TNF-R. The DNA can be truncated to
 CC produce sequences which express soluble receptor comprising
 CC residues 1-235, 1-185 or 1-163 of the protein.
 CC See also AAR11142.
 XX
 SQ Sequence 461 AA;

Query Match 100.0%; Score 2468; DB 12; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1e-152;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHAHALPAQVAFPTPYAPEGSTCRLREYYDQTQMCCSKSPG 60
 Db 1 mapvavwaalavglelwaahaalpaqvafptpyapegstcrlreydqtqmccskspg 60
 QY 61 QHAKVFCSTKSDTWCDSCESTVTLWNWVPECLSCSGSSDOVETQACTREONRICTC 120
 Db 61 qhakvfctksdtwcdscestvtqlwnwvpeclscsgssdovetqactreqnrietc 120
 QY 121 RPYGWCALSKQEGCRLCAPLKRCPGFGVAPGTETSDVVCPCAPGTFSTSTSDICR 180
 Db 121 rpygwcalskqegcrlcaplkrpfgfgvartetdvvcpcapgtfststsdicr 180
 QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLFPQVSTRSQHTQPTPEPSTAPSTS 240
 Db 181 phqicnvvaipgnasmdavctstsptrsmapgavhlfpqvstrsqhtqptpepstapsts 240
 QY 241 FLPLPMGPSPAEGSTGDFALPVGLIVCVTALGLLIIIGVNCVIMTVQKKPLCLQREAKV 300
 Db 241 flplpmgspspaegstgdfalpvglivcvtalglilliigvncvintvqkkplclqreakv 300
 QY 301 PHLPADKARQTQGPQOHLILITAPSSSSSSLESSASALDRRAPTRNOPQPGVEASGAGE 360
 Db 301 phlpadkarktqgpqohlilitapsssssslessasaldraptrnopqpgveasage 360
 QY 361 ARASTGSSDSSPGHGTVQNVVTCIVNCSSDISSQCSQASSTMGDTDSPSPSPKDEQ 420
 Db 361 arastgssdspghgtvqnvvtcivncssdissqcsqasstmgdtdspspspkdeq 420
 QY 421 VPESKEECAPRSOLETPETLLGSTEELPLGLVPDAGMKPS 461
 Db 421 vpskeecaprsoletpetllgsteeplplgvpdagmkps 461

RESULT 2
 AAR42058
 ID AAR42058 standard; Protein; 461 AA.
 XX
 AC AAR42058;
 XX
 DT 29-APR-1994 (first entry)
 XX
 DE Fibroblast derived TNF-R.
 XX
 KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
 KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
 KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;

KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
 KW graft verses host disease; sepsis; inflammation; allergy;
 KW autoimmune dysfunction.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22 /note= "Signal peptide"
 FT Protein 23..461 /note= "Mature hTNF-R"
 FT Peptide 23..185 /note= "Preferred soluble TNF-R"
 FT Peptide 23..207 /note= "Preferred soluble TNF-R"
 FT Peptide 23..257 /note= "Preferred soluble TNF-R"
 FT Peptide 23..206 /note= "Preferred soluble TNF-R"
 FT Peptide 23..204 /note= "Preferred soluble TNF-R"
 FT Peptide 1..206 /note= "Preferred soluble TNF-R"
 FT Peptide 1..204 /note= "Preferred soluble TNF-R"
 XX WO9319777-A.
 XX 14-OCT-1993.
 XX 26-MAR-1993; 93WO-US02938.
 XX 30-MAR-1992; 92US-0860710.
 XX (IMMUNEX CORP.
 XX Smith CA;
 XX WPI: 1993-336592/42.
 DR N-PSDB; AAQ49931.
 XX
 PT New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
 XX
 PS Claim 5; Fig 2; 85pp; English.

The sequences given in AAR42058-59 represent human tumour necrosis factor receptor (TNF-R) and the sequences in AAR42060-61 represent human interleukin-1 receptor (IL-1R). These sequences were used in the production of a fusion protein which conformed to one of the formulae:
 TNF-R-linker-TNF-R-linker-IL-1R
 IL-1R-linker-TNF-R-linker-TNF-R or
 TNF-R-linker-TNF-R
 The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moieties by such a distance that each component of the fusion protein is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causative role. They may be used to treat cachexia, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and autoimmune dysfunctions.

Sequence 461 AA;

Query Match 100.0%; Score 2468; DB 14; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1e-152;

```
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVATPYAPPEGSTCRLEYYDQTAQMCCKSPG 60
DB 1 mapvavmaalavglelwaahaalpaqvatpyapegstcrleyydqtamccskcspg 60
QY 61 QHAKVFCTKTSDDTCDSCEDSTYTLQNMWVPECLSGSRCSDDQVETQACTRQNRCTC 120
DB 61 qhakvfctktsdtdcdscdstytlqnmwvpeclsgsrccsdqvetqactreqnrietc 120
QY 121 RFGWYCALSKQEGCRICAPLRKCRPGFVGVARPGTETSDVWCKPCAPGTFSTNTSTDICR 180
DB 121 rfgwycalskqegcrlcaplrkcrpgfvgvarpgtetsdvwckpcapgtfntstsdicr 180
QY 181 PHQICNVVAIPGNASMDVACTSTPTRSMAPGAVHLPQPVSTRSQHTOPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasmdavctstptrsmapgavhlpqpvstrsqhtoptpepstapsts 240
QY 241 FLPLMGPSPPAEGSTGDFALPVLGIVGTALGLLIIGVNVCMVMTQVKKKPLCLQREAKV 300
DB 241 flplmgpsppaegstgdfalpvlgivgtalgliliigvncvmtqvkkkplclqreakv 300
QY 301 PHLPADKARGTQGEQHLITAPSSSSLESSASALDRRAPTRNQPAQVGEASGAGE 360
DB 301 phlpadkargtggeqhlitapsssslessasaldrraptrnqpapqvgveasgag 360
QY 361 ARASTGSSDSSPGCGHTQVNVTCIVNVWCSHSSQASSTMGDTSSSPSEPKDEQ 420
DB 361 arastgssdsspgghgtqvnvtcivnvcsdhssqcsqasstmgdtdsspsespkd 420
QY 421 VPFSKECAFRSQLETPETLLGSTEELKPLGLGVPDAGMKPS 461
DB 421 vpfskeecafrsqletpetllgsteekplglgvpdagmkps 461

RESULT 3
AAB18717
ID AAB18717 standard; Protein: 461 AA.
XX
AC AAB18717;
XX
DT 22-JAN-2001 (first entry)
XX
DE A human tumour necrosis factor family receptor (TNF-RII).
XX
KW Human; tumour necrosis factor family receptor; TNF; tumour growth;
KW cell proliferation; chlamydia infection; immunodeficiency; septic shock;
KW T-cell mediated autoimmune disease; acquired immunodeficiency syndrome;
KW AIDS; cerebral malaria; graft rejection; cytotoxicity; cachexia;
KW apoptosis; inflammation; cancer; cardiovascular disease; angiogenesis;
KW inflammatory disease; atherosclerosis; diabetes mellitus; allergy;
KW neurological disorder; autoimmune disease; wound healing; bone formation;
KW osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200054651-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-0056592.
XX
PR 15-MAR-1999; 99US-0124489.
XX
PR 26-MAY-1999; 99US-0136248.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Greene JM, Fleischmann RD, Ni J;
XX
DR WPI: 2000-618858/59.
XX
PT Novel tumour necrosis factor family receptor for diagnosing and treating
PT acquired immunodeficiency syndrome, cancer, cardiovascular diseases,
```

```
PT Inflammatory diseases and autoimmune diseases -
XX
PS Claim 16; Page 24-25; 228pp; English.
XX
CC The present sequence encodes human tumour necrosis factor family
CC receptor (TNF-RII) polypeptide. The specification describes a TNF
CC receptor designated TNF. An agonist to the TNF receptor is useful for
CC inhibiting tumour growth, to stimulate human cellular proliferation, to
CC regulate immune response and antiviral response, to protect against the
CC effects of ionising radiations, to protect against chlamydia infections,
CC to regulate growth, and to treat immunodeficiencies such as in human
CC immunodeficiency virus (HIV). An antagonist to the TNF receptor is
CC useful for treating T-cell mediated autoimmune diseases, acquired
CC immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft
CC rejection, cytotoxicity, cachexia, apoptosis, and inflammation. TNF
CC polynucleotides and polypeptides, and TNF agonists and antagonists
CC are useful for treating cancers, cardiovascular diseases, inflammatory
CC diseases, atherosclerosis, diabetes mellitus, neurological disorders,
CC autoimmune diseases, for promoting angiogenesis, for treating allergy,
CC for wound healing, for regulating bone formation and for treating
CC osteoporosis.
XX
SQ Sequence 461 AA;
Query Match 100.0%; Score 2468; DB 21; Length 461;
Best Local Similarity 100.0%; Pred. No. 1e-152;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVATPYAPPEGSTCRLEYYDQTAQMCCKSPG 60
DB 1 mapvavmaalavglelwaahaalpaqvatpyapegstcrleyydqtamccskcspg 60
QY 61 QHAKVFCTKTSDDTCDSCEDSTYTLQNMWVPECLSGSRCSDDQVETQACTRQNRCTC 120
DB 61 qhakvfctktsdtdcdscdstytlqnmwvpeclsgsrccsdqvetqactreqnrietc 120
QY 121 RFGWYCALSKQEGCRICAPLRKCRPGFVGVARPGTETSDVWCKPCAPGTFSTNTSTDICR 180
DB 121 rfgwycalskqegcrlcaplrkcrpgfvgvarpgtetsdvwckpcapgtfntstsdicr 180
QY 181 PHQICNVVAIPGNASMDVACTSTPTRSMAPGAVHLPQPVSTRSQHTOPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasmdavctstptrsmapgavhlpqpvstrsqhtoptpepstapsts 240
QY 241 FLPLMGPSPPAEGSTGDFALPVLGIVGTALGLLIIGVNVCMVMTQVKKKPLCLQREAKV 300
DB 241 flplmgpsppaegstgdfalpvlgivgtalgliliigvncvmtqvkkkplclqreakv 300
QY 301 PHLPADKARGTQGEQHLITAPSSSSLESSASALDRRAPTRNQPAQVGEASGAGE 360
DB 301 phlpadkargtggeqhlitapsssslessasaldrraptrnqpapqvgveasgag 360
QY 361 ARASTGSSDSSPGCGHTQVNVTCIVNVWCSHSSQASSTMGDTSSSPSEPKDEQ 420
DB 361 arastgssdsspgghgtqvnvtcivnvcsdhssqcsqasstmgdtdsspsespkd 420
QY 421 VPFSKECAFRSQLETPETLLGSTEELKPLGLGVPDAGMKPS 461
DB 421 vpfskeecafrsqletpetllgsteekplglgvpdagmkps 461

RESULT 4
AAB11001
ID AAB11001 standard; Protein: 461 AA.
XX
AC AAB11001;
XX
DT 13-MAY-1991 (first entry)
XX
DE 40kd TNF inhibitor precursor.
XX
KW Tumour necrosis factor; Inhibitor.
```

XX OS Homo sapiens.
XX PN AU9058976-A.
XX PD 24-JAN-1991.
XX PF 16-JUL-1990; 90AU-0058976.
XX PR 07-FEB-1990; 90US-0479661.
XX PR 18-JUL-1989; 89US-0381080.
XX PR 11-DEC-1989; 89US-0450329.
XX PA (SYNE-) SYNERGEN INC.
XX WPI; 1991-073847/11.
XX DR N-PSDB; AAQ10907.
XX PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
XX and -beta, useful as therapeutic agent.
XX PS Disclosure; Fig 39; 142pp; English.
XX CC The sequence comprises the entire 40 kD TNF inhibitor. The clone
CC from which the sequence was deduced was isolated from a cDNA
CC library prep. from RNA form U937 cells treated with PMA/PHA.
CC The whole gene can be inserted into expression vectors for prepn.
CC of TNF inhibitor for use in the treatment of inflammatory and
CC degenerative diseases.
CC See also AARI0986 and AARI0984.
XX
XX SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 12; Length 461;
Best Local Similarity 99.8%; Pred. No. 2.6e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPPGSTGRLREYDQTAQMCCSKCSPG 60
DB 1 mapvavaaalavglelwaaahalpavaftpyapepgstgrlreydydqtaqmccskcspg 60
QY 61 QHAKVFCTKTSRDVCDSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTC 120
DB 61 qhakvfctktsrdvcdscdstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120
QY 121 RPYWYCALSKQEGCRICAPLRKCRPGFVARPGTETSDVVKCPACPTFSNTSSTDICR 180
DB 121 rpywycalskqegcrlicaplrkcrpgfvarpgtetdsvvckpcapgtfsntssdtdicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQVPVSTRSOHTQPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasmdavctstsptrsmapgavhlpqvpvstrsqhtqptpepstapsts 240
QY 241 FLPLPMGFPSPAEGSTGDFALFVLGVGTALGGLLIIGVWNCVINTQVKKPLCLQREAKV 300
DB 241 flplpmgfpspaegstgdfalpvglvgvtalgglligvncvintqvkplclqreakv 300
QY 301 PHLPADKARTQGPQQHLLITAPSSSSSLESASALDRRAPTRNQPQAPGVEASGAGE 360
DB 301 phlpadkargtqgpeqqhllitapsssslessasaldraptrnqpqpgveasgag 360
QY 361 ARASTGSSDSSPGHGCTGVNVTCTVNVVCSDDHSSQSSQASSTMGDTDSPPSPKDEQ 420
DB 361 arastgssdsspghgctgvnvtctvnnvcsddhssqssqassmgdtdspspspkdeq 420
QY 421 VPFSKECAPRSOLETPETLLGSTEKPLPLGVPDAGMKPS 461
DB 421 vpfskecaprsoletpetllgstekplplgvpdagmkps 461

RESULT,
AAB37801

ID XX AAB37801 standard; Protein; 461 AA.
AC XX AAB37801;
DT XX 23-FEB-2001 (first entry)
DE XX Human tumour necrosis factor p75 receptor.
XX KW Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW chronic myelogenous leukaemia; inflammatory bowel disease.
OS Homo sapiens.
XX PN WO2000064479-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-US11700.
XX PR 27-APR-1999; 99US-0301274.
XX PA (ANTI-) ANTIBODY SYSTEMS INC.
XX PI Fredeking TM, Ignatyev GM;
XX WPI; 2000-679646/66.
XX
XX PT Novel compositions comprising tetracycline or tetracycline-like
XX compounds for the treatment and/or prevention of acute inflammatory
XX responses and diseases, e.g. septic shock and immune complex-induced
XX colitis -
XX PS Disclosure; Page 169-171; 183pp; English.
XX CC The present sequence is given in a specification relating to novel
XX compositions and methods containing tetracycline or tetracycline-like
XX compounds for treating and/or preventing acute inflammatory responses and
XX diseases. Such diseases include acute inflammatory conditions associated
XX with viral haemorrhagic diseases (including diseases caused by
XX Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
XX parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
XX disorders, acute cardiovascular events, chronic myelogenous leukaemia and
XX transplanted bone marrow-induced graft-versus-host disease, septic shock,
XX immune complex-induced colitis, cerebrospinal fluid inflammation,
XX multiple sclerosis, inflammatory responses associated with trauma,
XX systemic inflammatory response syndrome (SIRS), adult respiratory
XX distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
XX and Crohn's disease.
XX SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 21; Length 461;
Best Local Similarity 99.8%; Pred. No. 2.6e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPPGSTGRLREYDQTAQMCCSKCSPG 60
DB 1 mapvavaaalavglelwaaahalpavaftpyapepgstgrlreydydqtaqmccskcspg 60
QY 61 QHAKVFCTKTSRDVCDSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTC 120
DB 61 qhakvfctktsrdvcdscdstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120
QY 121 RPYWYCALSKQEGCRICAPLRKCRPGFVARPGTETSDVVKCPACPTFSNTSSTDICR 180
DB 121 rpywycalskqegcrlicaplrkcrpgfvarpgtetdsvvckpcapgtfsntssdtdicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQVPVSTRSOHTQPTPEPSTAPSTS 240

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Db 181 phqicnvvaipgnasrdavctstpsrmapgavhlpqpvstrsqtqtpepstapsts 240
QY 241 FLPLPKGSPPAEGSGTDFALPVLGVVTAALGLLIIGVNVVIMTQVKKPKLCLOREAKV 300
Db 241 flpmpgspgaegsgtdfalpvgvltalglilgvvncvmtqvkpkpklclqreakv 300
QY 301 PHLPADKARGTQGPQEQHLLITAPSSSSLESSASALDRRAPTRNOAPGVEASGAGE 360
Db 301 phlpadkargtgqpeqghllitapsssslessasaldrraptrnqpapgyeasgag 360
QY 361 ARASTGSSDSSPGHGHTQVNVVTCIVNVCSDDHSSQCSQASSTMGDTSSSPSEPKDEQ 420
Db 361 arastgssdsspgghgtqvnvtciinvncssdhssqcsqasstmgdtsspsespkd 420
QY 421 VPFSKECAFRRSQLETPETLLGSTEKPLPLGVDPDAGMKPS 461
Db 421 vpfskecafrsqletpetllgsteekplplgvdpdagmkps 461

```

RESULT 6

AAB01342
ID AAB01342 standard; Protein; 461 AA.

XX AC AAB01342;

XX DT 25-SEP-2000 (first entry)

XX DE Death receptor.

XX KW UL144; death receptor; apoptosis; programmed cell death; FAS;
KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW human.

XX OS Homo sapiens.

XX PN WO200034335-A2.

XX PD 15-JUN-2000.

XX PF 03-DEC-1999; 99WO-US26035.

XX PR 04-DEC-1998; 98US-0205018.

XX PA (SCHE) SCHERING CORP.

XX PI Leong C, Phillips JH;

XX DR WPI; 2000-423383/36.

XX PT Purified or recombinant polypeptide for modulating apoptosis comprises
PT a sequence which binds to an antibody specific for UL144 or its
PT fragments

XX PS Disclosure; Page 74-75; 76pp; English.

XX CC A pure or recombinant polypeptide which binds to a polyclonal antibody
CC specific for the mature UL144 is useful for screening molecules which
CC block induction of apoptosis or interfere with antiapoptotic activity.
CC The polypeptide is also useful for modulating apoptosis and useful in
CC treatment of conditions associated with abnormal physiology or
CC development, such as cancer or degenerative conditions and for
CC regulation of viral infection and replication. At least five
CC different death receptors are known, which include the CD95
CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.

XX SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 21; Length 461;
Best Local Similarity 99.8%; Pred. No. 2.6e-152;

```

Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPPEGSTCRRLREYDQTAOMCCSKCSPG 60
Db 1 mapvavaaalavglelwaahahalpaqvaftpyappegstcrrlreyddqtaomccskcspg 60
QY 61 QHAKVFCTKTSDTVCDSCEDSTYTQLMNWVPECLSGSRCSDDQVETQACTREQNRICTC 120
Db 61 qhakvfctktsdtvcdscedstytqlmnwvpeciscgrcsddqvetaqctreqnrictc 120
QY 121 RPYWYCALSKQEGRCRLCAPLRKCRPGFVAPRGVETSDVCKPCAPGTFNTTSTDTICR 180
Db 121 rpywycalskqegrcrlcaplrkcrpgfvgvargtetsdvckpcapgtfnttsatdicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAGAVHLPQPVSTRSOHTQTPPEPSTAPSTS 240
Db 181 phqicnvvaipgnasrdavctstpsrsmagavhlpqpvstrshtqtptpepstapsts 240
QY 241 FLPLPMGSPPAEGSGTDFALPVLGVVTAALGLLIIGVNVVIMTQVKKPKLCLOREAKV 300
Db 241 flpmpgspgaegsgtdfalpvgvltalglilgvvncvmtqvkpkpklclqreakv 300
QY 301 PHLPADKARGTQGPQEQHLLITAPSSSSLESSASALDRRAPTRNOAPGVEASGAGE 360
Db 301 phlpadkargtgqpeqghllitapsssslessasaldrraptrnqpapgyeasgag 360
QY 361 ARASTGSSDSSPGHGHTQVNVVTCIVNVCSDDHSSQCSQASSTMGDTSSSPSEPKDEQ 420
Db 361 arastgssdsspgghgtqvnvtciinvncssdhssqcsqasstmgdtsspsespkd 420
QY 421 VPFSKECAFRRSQLETPETLLGSTEKPLPLGVDPDAGMKPS 461
Db 421 vpfskecafrsqletpetllgsteekplplgvdpdagmkps 461

```

RESULT 7

AAB35331
ID AAB35331 standard; Protein; 461 AA.

XX AC AAB35331;

XX DT 08-MAY-2001 (first entry)

XX DE Human TNF receptor SEQ ID NO: 6.

XX KW Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.

XX OS Homo sapiens.

XX PN WO200105834-A1.

XX PD 25-JAN-2001.

XX PF 14-JUL-2000; 2000WO-US19343.

XX PR 16-JUL-1999; 99US-0144087.

XX PR 18-AUG-1999; 99US-0149450.

XX PR 20-AUG-1999; 99US-0149712.

XX PR 10-SEP-1999; 99US-0153089.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Ni J, Young PE;

XX DR WPI; 2001-112682/12.

XX PT Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides (TR13) and (TR14), useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
XX hypohidrotic ectodermal dysplasia -

```
PS Disclosure; Page 377-378; 418pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC useful in the diagnosis and treatment of many diseases, including cancer,
CC autoimmune diseases, cardiovascular disorders, allergies, aneurysms and
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC infections.
XX
SQ Sequence 461 AA;

Query Match          99.8%; Score 2462; DB 22; Length 461;
Best Local Similarity 99.8%; Pred. No. 2.6e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPVAVWAALAVGLELWAAHAHALPAQVAFTPYAPPEGSTCRLREYVDQTAQMCCSKCSPG 60
Db 1 mapvavwaalavglelwaahaahalpaqvaftpyapegstcrlreydydtaqmccskcspg 60
Qy 61 QHAKVFCFKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDVETQACTREQNRICTC 120
Db 61 qhakvfcfktsdtdvcdscdstytqlwnwvpeclscgsrcsddvetaqactreqnrictc 120
Qy 121 RPYWCALSKQEGRCRLCAPLKRCPGFGVAPRGTTSDVWCKPCAPGTFTSNTSTDICR 180
Db 121 rpywcalskqegrcrlcaplkrkrcpgfgvargttsdvwckpcapgtftsntstdicr 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPPQVSTRSQHTQTPPEPSTAPSTS 240
Db 181 phqicnvvaipgnasmdavctstptrsmapgavhlppqvstrsqhtqtppepstapsts 240
Qy 241 FLPMGSPPPAEGSTGDFALPVGVLIVGTALGLLIIGVNVCIMTVQVKKPLCLQREAKV 300
Db 241 flpmgspppaegstgdfalpvgvlivgtalglilliigvncvmtqvkkpklclqreakv 300
Qy 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQOPAGVEASGAGE 360
Db 301 phlpadkargtgpgqgqhlhitapsssssslessasaldraptrnqpapgvveasgag 360
Qy 421 VPESKECAPRSOLETPTLLGSTEKPLPLGVDPAGMKPS 461
Db 421 vpskecaprsqletptllgstekplplgvdpagmkps 461

RESULT 8
AAB36698
ID AAB36698 standard; Protein: 461 AA.
XX
AC AAB36698;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor TNFR2 protein SEQ ID NO:3.
XX
KW Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neutrotic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW immunosuppressive; neutrotic; anti-HIV; antiparkinsonian;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
OS Homo.sapiens.
XX
PN WO200071150-A1.
XX
PD 30-NOV-2000.
```

```
XX 18-MAY-2000; 2000WO-US13515.
XX
XX 20-MAY-1999; 99US-0135164.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX
XX WPI; 2001-041051/05.
XX
XX Nucleic acid encoding a TR1D polypeptide, also referred to as tumor
XX necrosis factor receptor 5, useful in the diagnosis, treatment or
XX prevention of cancer, autoimmune disorders and viral infection -
XX
XX Disclosure; Fig 2; 285pp; English.
XX
XX The present invention describes the human TR1D protein (tumour necrosis
XX factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
XX intracellular domain, also referred to as tumour necrosis factor
XX receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive,
XX neutrotic, neutrotective, antiviral, antiinflammatory, anticonvulsant,
XX antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
XX activities, and can be used in gene therapy. The TR1D polynucleotides
XX are useful for detecting complementary polynucleotides. TR1D proteins and
XX polynucleotides are useful in the treatment of tumours, resistance to
XX parasite, bacteria and viruses, restenosis and graft versus host disease.
XX They are also useful for inducing proliferation of T-cells, endothelial
XX cells and certain hematopoietic cells, to regulate antiviral responses
XX and to prevent certain autoimmune diseases after stimulation of TR1D by
XX an agonist or TRAIL binding facilitator. The antibodies which bind TR1D
XX polypeptides are useful for treating and/or preventing diseases
XX associated with increased or decreased apoptotic cell death. The TR1D
XX polynucleotides, proteins, antibodies, agonists and antagonists are
XX useful in the diagnosis, treatment or prevention of: (a) cancer;
XX (b) autoimmune disorders; (c) diseases associated with increased
XX apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
XX present sequence represents a tumour necrosis factor receptor used in
XX comparison with TR1D in the exemplification of the present invention.
XX
SQ Sequence 461 AA;

Query Match          99.8%; Score 2462; DB 22; Length 461;
Best Local Similarity 99.8%; Pred. No. 2.6e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPVAVWAALAVGLELWAAHAHALPAQVAFTPYAPPEGSTCRLREYVDQTAQMCCSKCSPG 60
Db 1 mapvavwaalavglelwaahaahalpaqvaftpyapegstcrlreydydtaqmccskcspg 60
Qy 61 QHAKVFCFKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDVETQACTREQNRICTC 120
Db 61 qhakvfcfktsdtdvcdscdstytqlwnwvpeclscgsrcsddvetaqactreqnrictc 120
Qy 121 RPYWCALSKQEGRCRLCAPLKRCPGFGVAPRGTTSDVWCKPCAPGTFTSNTSTDICR 180
Db 121 rpywcalskqegrcrlcaplkrkrcpgfgvargttsdvwckpcapgtftsntstdicr 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPPQVSTRSQHTQTPPEPSTAPSTS 240
Db 181 phqicnvvaipgnasmdavctstptrsmapgavhlppqvstrsqhtqtppepstapsts 240
Qy 241 FLPMGSPPPAEGSTGDFALPVGVLIVGTALGLLIIGVNVCIMTVQVKKPLCLQREAKV 300
Db 241 flpmgspppaegstgdfalpvgvlivgtalglilliigvncvmtqvkkpklclqreakv 300
Qy 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQOPAGVEASGAGE 360
Db 301 phlpadkargtgpgqgqhlhitapsssssslessasaldraptrnqpapgvveasgag 360
Qy 361 ARASTGSSDSSPGGHGCTQVNVTCIVNVCSSSDHSSQCSQASSTMGDTDSSSPSPKDEQ 420
Db 361 arastgssdsspgghgctqvnvtcivnvcsssdhssqcsqasstmgdtdssspspkdeq 420
```

```

Db 361 arastgssdsspghgtqvnvtciwnvcssdhssqscssqasstmgtdsspsespkdq 420
Qy 421 VPFSEKCAFRLQLETPETLLGSTEELKPLPLGVDPDAGMKPS 461
Db 421 vpfsekecafrsqtletpetllgsteeekplplgvdpdagmkps 461

RESULT 9
AAB37686
ID AAB37686 standard; Protein; 461 AA.
XX
AC AAB37686;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 40 kDa TNF inhibitor precursor.
XX
KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human; lymphotoxin.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.
XX
PF 19-JAN-1995; 95US-0375242.
XX
PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
PA (AMGE-) AMGEN INC.
XX
PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
DR WPI; 2001-006443/01.
DR N-PSDB; AAC83951.
XX
PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF.
XX
PS Example 12; Fig 39; 82pp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is the precursor for 40 kDa TNF inhibitor. The 40 kDa
CC TNF inhibitor can inhibit both TNF alpha and beta (lymphotoxin).
XX
SQ Sequence 461 AA:

Query Match 99.8%; Score 2462; DB 22; Length 461;
Best Local Similarity 99.8%; Pred. No. 2.6e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPVAWAAALVGLLEWAAHALPAQVATPYAPPGSTCRLEYYDYDTQAQMCCKSCSPG 60
Db 1 mapvawaaalvglelwaaahalpavqatpyapepgstcrleyydydtqamccskspg 60
Qy 61 QHAKVCTKTSVTCDSCESTYTLQWNVWPECLSCGSRCSDDVETQACTREONRICTC 120
Db 61 qhakvctktsdvcdscdstytlqwnvwpeclscgsrcssddvqetqactreqrictc 120
Qy 121 RPYWCALSKQEGCRLCAPLRKCRPGFGVAPFGTETSDVVKPCAPGTFSTNTTSTSDICR 180

```

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Db 121 rpywcalskqegcrclcaplrkcrpgfgvapggtetdvckpcapgtfnttstsdicr 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSOHTQPTPEPSTAPSTS 240
Db 181 phqicnvvaipgnasrdavctstsptrsmagavhlppqpvstrsqhtqptpepstapsts 240
Qy 241 FLIPMGSPPEAGSTGDFALPVGILIVGTALGLLIIIGVNVNCVIMTVQVKKKPLCLQREAKV 300
Db 241 flipmgsppeagstgdfaipvgilivgtalglilivgvncvimtqvkklplclqreakv 300
Qy 301 PHLPADKARGTQGPQOHLITAPSSSSSSLESSASALDRRAPTRNOAPQPCVEASGAGE 360
Db 301 phlpadkargtqgpeqhlitapsssssslessasaldrraptrnqpqagveasgagage 360
Qy 361 ARASTGSSDSPGHHGTQVNVVTCIVNVCSSSHSSQSCSSQASSTMGDTDSSPESPCKDEQ 420
Db 361 arastgssdspgghgtqvnvtciwnvcssdhssqscssqasstmgtdcsspsespckdeq 420
Qy 421 VPFSEKCAFRLQLETPETLLGSTEELKPLPLGVDPDAGMKPS 461
Db 421 vpfsekecafrsqtletpetllgsteeekplplgvdpdagmkps 461

RESULT 10
AAR72504
ID AAR72504 standard; Protein; 461 AA.
XX
AC AAR72504;
XX
DT 31-OCT-1995 (first entry)
XX
DE p75 Tumour Necrosis Factor Receptor.
XX
KW Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
KW receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 27..214
FT Domain /label= TBP11.
FT Domain 258..285
FT Misc-difference 259
FT /note= "Unidentified amino acid."
XX
PN EP648783-A.
XX
PD 19-APR-1995.
XX
PF 11-OCT-1994; 94EP-0116015.
XX
PR 12-OCT-1993; 93IL-0107267.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
PA (WALL/) WALLACH D.
XX
PI Beletsky I, Bigda J, Mett I, Wallach D;
XX
DR WPI; 1995-148673/20.
DR N-PSDB; AAQ89544.
XX
PT Tumour necrosis factor (TNF) receptor ligand - used to increase
PT inhibitory effect of a soluble TNF receptor
XX
PS Disclosure; Figure 2; 18pp; English.
XX
CC A ligand to a member of the tumour necrosis factor (TNF)/nerve
CC growth factor (NGF) receptor family which binds either to the region
CC of the 4th-Cys rich domain of the receptor, or to the region between
CC it and the cell membrane may be used in the production of a
CC pharmaceutical composition for increasing the inhibitory effect of a

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CC soluble receptor of the TNF/NGF receptor family. This sequence
CC is the sequence of the p75 TNF receptor.
XX
SQ Sequence 461 AA;

Query Match 97.0%; Score 2394; DB 16; Length 461;
Best Local Similarity 96.4%; Pred. No. 6.7e-148;
Matches 451; Conservative 0; Mismatches 3; Indels 14; Gaps 2;

QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLEYDQTAQMCCSKCSPG 60
DB 1 mapvavwaalavglelwaahalpaqvaftpyapepgstcrleydqtacmccskcspg 60
QY 61 QHAKVFCTKTSDTVCDCSDSTYTLQNNWVPECLSCGRSSDQVETQACTREQNRICTC 120
DB 61 qhakvfctktsdtdvcdscedstytqlnnwvpeclscgrssdqvetaqactreqnrictc 120
QY 121 RPYGWCALSKOEGRCRLCAPLRKCRPGFVARPGTETSDVWCKPCAPGTFSTNTSTDICR 180
DB 121 rpygwcalskqegrcrlcaplrkcrpgfvarpgtetsdvwckpcapgtfstntstdicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPCAVHLPOPVSTRSQHTQPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasmdavctstptrsmapcavhlbpqvstrsqhtqptpepstapsts 240
QY 241 FLLPMGPPPAEGSTGDFALPVGLIVGTALGLLIIGVNCVIMTVQVKKPLCLQREAKV 300
DB 241 flpmgpppaegstgdfalpvglivgtalgliliigvncvmtqvkkplclqreakv 300
QY 301 PHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPTRNQPAQVGEASGAGE 360
DB 301 phlpadkargtqgpeqghllitapsssssslessasaldraptrnqpqavgeasgag 360
QY 361 ARASTGSSDSSPGGHGTQ-----VNVTCIVNVCSSDSSHSSQSSQASSTMGTDSSTS 413
DB 361 arastgssdspgghgtqapgvgeasvntctvnnvcssdshssqssqassumgtdssps 413
QY 414 ESPKDEOVFSEKECAPRSOLETPETLLGSTEEKPLPLGVDPDAGMKPS 461
DB 414 espkdeovfsekecaprsoletpetllgsteeekplplgvdpdagmkps 461

RESULT 11
AAR51002
ID AAR51002 standard; Protein; 461 AA.
XX
AC AAR51002;
XX
XX 07-OCT-1994 (first entry)
XX
DE Sequence of human tumour necrosis factor receptor type I
DE (TNFRI).
XX
XX Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal
FT Peptide 22..461
FT /label= mature
XX
XX W09406476-A.
XX
XX 31-MAR-1994.
XX
XX '14-SEP-1993; 93WO-US08666.
XX
XX 15-SEP-1992; 92US-0946236.
XX
XX (IMMUNEX ) IMMUNEX CORP.
XX
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XX Jacobs CA, Smith CA;
PI WPI; 1994-118172/14.
XX N-PSDB; AAO45224.
XX
XX Treating TNF mediated inflammatory diseases with TNF antagonist -
XX esp. soluble form of TNF receptor, opt. as fusion protein with
XX human immunoglobulin Fc region, esp. for treating arthritis
XX
XX Disclosure; Page 28-30; 47pp; English.
XX
XX AA045224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
XX cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
XX having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
XX TNFRI was described in Smith et al., Science 248:1019, 1990. Clone 1
XX is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
XX preferred TNFRs of the present invention are soluble forms of TNFRI
XX and TNFRII having at least 20 AAs. Soluble TNFR constructs are
XX devoid of a transmembrane region but retain the ability to bind TNF.
XX Examples of soluble TNFRs are huTNFRdelta235, huTNFRdelta185 and
XX huTNFRdelta163 which encode respectively AAs 1-235, 1-185 and 1-163
XX of AAR51002. An equivalent soluble TNFR is huTNFRdelta x wherein x
XX is selected from any one of AAs 163-235 of AAR51002.
XX
XX Sequence 461 AA;

Query Match 96.3%; Score 2376; DB 15; Length 461;
Best Local Similarity 96.7%; Pred. No. 9.9e-147;
Matches 446; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLEYDQTAQMCCSKCSPG 60
DB 1 mapvavwaalavglelwaahalpaqvaftpyapepgstcrleydqtacmccskcspg 60
QY 61 QHAKVFCTKTSDTVCDCSDSTYTLQNNWVPECLSCGRSSDQVETQACTREQNRICTC 120
DB 61 qhakvfctktsdtdvcdscedstytqlnnwvpeclscgrssdqvetaqactreqnrictc 120
QY 121 RPYGWCALSKOEGRCRLCAPLRKCRPGFVARPGTETSDVWCKPCAPGTFSTNTSTDICR 180
DB 121 rpygwcalskqegrcrlcaplrkcrpgfvarpgtetsdvwckpcapgtfstntstdicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPCAVHLPOPVSTRSQHTQPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasmdavctstptrsmapcavhlbpqvstrsqhtqptpepstapsts 240
QY 241 FLLPMGPPPAEGSTGDFALPVGLIVGTALGLLIIGVNCVIMTVQVKKPLCLQREAKV 300
DB 241 flpmgpppaegstgdfalpvglivgtalgliliigvncvmtqvkkplclqreakv 300
QY 301 PHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPTRNQPAQVGEASGAGE 360
DB 301 phlpadkargtqgpeqghllitapsssssslessasaldraptrnqpqavgeasgag 360
QY 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSDSSHSSQSSQASSTMGTDSSESFPKDDQ 420
DB 361 arastgssdspgghgtqvnvtcivnnvcssdshssqssqassmgtdsspsespkdq 420
QY 421 VPFSKECAPRSOLETPETLLGSTEEKPLPLGVDPDAGMKPS 461
DB 421 vpfskecaprsoletpetllgsteeekplplgvdpdagmkps 461

RESULT 12
AAY30935
ID AAY30935 standard; Protein; 392 AA.
XX
XX AAY30935;
XX
XX 18-OCT-1999 (first entry)
XX
```

DE Human tumour necrosis factor binding protein fragment.

XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW autoimmune glomerulonephritis; cerebral malaria; immune response;
KW antagonist; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..392

FT /note= "Partial sequence, no start codon given"

PN EP939121-A2.

XX 01-SEP-1999.

XX 31-AUG-1990; 90EP-0116707.

XX 20-APR-1990; 90CH-0001347.

PR 12-SEP-1989; 89CH-0003319.

PR 08-MAR-1990; 90CH-0000746.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

PI Schlaeger E;

XX WPI; 1999-480840/41.

DR N-PSDB; AAZ09171.

XX New insoluble proteins, and fragments, that bind to tumor necrosis

PT factor, used to treat e.g. septic shock or cerebral malaria

XX Claim 4a; Fig 4; 25pp; German.

PS This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (i) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence represents
CC a tumour necrosis factor binding protein fragment described in the method
CC of the invention.

XX Sequence 392 AA;

Query Match 83.1%; Score 2051.5; DB 20; Length 392;

Best Local Similarity 98.7%; Pred. No. 9.8e-126;

Matches 387; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 71 SDTVCDSCEDSTYTOLNMWVPECLSCGSCSSDQVETQACTREONRICRPGWYCALSK 130

Db 1 sdsdvcscdsstytqlwnwvpeclscgscscsdqvetqactreqnricrpgwycalsk 60

QY 131 QEGCRLCAPLKRCPGFGVARGPGETSTSDVCKPCAPGTFTSNTSDICRPHQICNVVAI 190

Db 61 qegcrlcaplkrpfgvargpgetstsdvckpcapgtftstsdicrphqicnvval 120

QY 191 PCNASMDVACTSTSTRMAPCAVHLPPQVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 250

Db 121 pgnardavctststrmapgavhlpqpvstrsqhtqpspepstapstsfllpmgsp 180

QY 251 AEGSTGDFALPGLVIGVTALGLLIIGVNVCVIMTQVKKKPLCLOREAKVPHLPADKARG 310

Db 181 aegstgdfalpgvlvgvtalglilggnvncvmtqvkklpcklqreakvphlpadkarg 240

QY 311 TQGPQQHLLITAPSSSSSSLESSASSALDRRAPTRNQOPAGVSEAGAEARASTGSS-D 369

XX

Db 241 tqgpeqghllitapsssssslessasaldraptrnqpqpgvseagagearastgssad 300

QY 370 SSGEGHGTQVNVTCIVNVCSHSSQCSQASSTMGDTSSPSESPPKDEQVPSKEBCA 429

Db 301 sspgghgtqvnvtcivnvcsdhssqcsqasstmgtdtsspsespkdqvpfskesca 360

QY 430 FRSQLETPETLLGSTERKPLPLGVDPDAGMKPS 461

Db 361 frsqletpetllgsteeekplplgvdpdagmkps 392

RESULT 13

AAR11605

ID AAR11605 standard; Protein; 392 AA.

XX AAR11605;

XX 24-MAY-1991 (first entry)

XX Human 75kD TNF-binding protein.

XX Tumour Necrosis Factor; binding proteins; septic shock;

XX autoimmune glomerulonephritis; lymphokine; cytokine.

XX Key Location/Qualifiers

FT Misc-difference 3 /label= Ser, Thr

XX EP417563-A.

XX 20-MAR-1991.

XX 31-AUG-1990; 90EP-0116707.

XX 20-APR-1990; 90CH-0001347.

PR 12-SEP-1989; 89CH-0003319.

PR 08-MAR-1990; 90CH-0000746.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

PI Schlaeger EJ;

XX WPI; 1991-081851/12.

DR N-PSDB; AAQ10956.

XX Insoluble tumour necrosis factor binding proteins - and DNA

PT encoding them, useful in pharmaceutical prods. and for antibody

PT prodn.

XX Claim 1; Fig 1; 26pp; German.

XX Partial amino acid sequences were determined for the 55 and 75kD

CC TNF-BPs (see AAR1072-R11081) and oligonucleotide primers were used

CC synthesised based on these partial sequences. The primers were used

CC to produce a cDNA fragment for use as a probe to screen a human

CC placental cDNA bank constructed in lambda gt11. Positive clones were

CC identified and sequenced. Repeated sequencing showed a discrepancy

CC at position 7 such that the third codon encodes either Thr or Ser.

CC See also AAQ10955.

XX Sequence 392 AA;

Query Match 83.1%; Score 2050.5; DB 12; Length 392;

Best Local Similarity 98.7%; Pred. No. 1.1e-125;

Matches 387; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 71 SDTVCDSCEDSTYTOLNMWVPECLSCGSCSSDQVETQACTREONRICRPGWYCALSK 130

Db 1 sdsdvcscdsstytqlwnwvpeclscgscscsdqvetqactreqnricrpgwycalsk 60

QY 131 QEGCRLCAPLKRCPGFGVARGPGETSTSDVCKPCAPGTFTSNTSDICRPHQICNVVAI 190

Example 13; Fig 10; 72pp; English.

The present sequence is a fusion protein of tumour necrosis factor receptor (TNFR) and the constant region of an immunoglobulin molecule (Fc), denoted *spNFR*(075)*Fc*. A recombinant adeno-associated virus (rAAV) vector encoding the present sequence was used to infect a rat model of arthritis. The rats showed a significant reduction in arthritis symptoms compared with control groups. This was performed as an example illustrating an invention providing a new recombinant viral vector. The vector comprises a single-stranded heterologous nucleotide sequence having a region that forms intrastand base pairs so that the expression of a coding region of the heterologous sequence is enhanced. The recombinant viral vector is useful in gene therapy and genomics screening. The vectors may also be used in the transfection, transduction and expression of a sequence of interest in a host cell and in the manufacture of a medicament for treatment. The time required for the accumulation of the gene product of interest is reduced to days rather than weeks since the vectors can efficiently and rapidly form duplex templates for transcription.

Sequence 518 AA;

Query Match	58.1%	Score 1433;	DB 22;	Length 518;
Best Local Similarity	64.5%;	Pred. No. 2e-85;		
Matches	289;	Conservative	22;	Mismatches 67; Indels 70; Gaps 10;
QY	1	MAPVAVWAALAVGLELWAAAHALPAQVAFPPYAPEPGSTCRLREYYDQTAMCCKSKSPG	60	
Db	30	mapvavwaalavglelwaahaalpaqvafppypepgstcrlreyydqtamcckskspg	89	
QY	61	QHAKVFTCKTSDTVCDSCEDBSTYTLQNNWVPECLUSCRGSSDDQVETACPRQNRICTC	120	
Db	90	qhakvftcktsdtvcdscedstytqlwnwpeclscrgssddveqaccreqnricctc	149	
QY	121	RPGWYCALSKQEGRLCAPLRKCRPGFGVARGPTETSDVWCKPCAPGTFSTTSSDTCIR	180	
Db	150	rpwycaalskqegrlcaplrkerpgfgvargptetsdvwckpcapgtfsttsttdcir	209	
QY	181	PHQICNVVAITPGNASMDAVCTSTSPTRSMAPGAVHLPQVSTRSOHTQPTPEPSTAPSTS	240	
Db	210	phqicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts	269	
QY	241	FLIPMGSPSPAEGSTGDFALPVLGLIVGTALGLLIIIGVWNCVIMTQVKKKPLCLQREAKV	300	
Db	270	flipmgspspaegstgdfalpvlgliivgtalglilliigvwncvimtqvkkkplclqreakv	297	
QY	301	PHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAP-----TRNQPG--	349	
Db	298	ppcpapelgg--gps-----vflfppkpkdtlmis-----rtpevtcvvvdvshdpevk	345	
QY	350	----APGVEASGAEARACTGSSDSPGGHGTQVNTVCITNVN-----CSSSDHSSQSSQKA-S	402	
Db	346	fnwyvdgvevh----naktkpreegynstyrvsvitvlhqdwlngkdyckkyvsnkalp	400	
QY	403	STMGDDTSSPSESPKDEQV-----PFSKEE	427	
Db	401	apmaktiskakqgpreqvvtlppsrdc	428	

Search completed: February 12, 2002, 12:47:38
Job time: 160 sec

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OM protein - protein search, using sw model

Run On: February 12, 2002, 12:45:28 ; Search time 15.87 Seconds
(without alignments)
653.687 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEKPLPLGVDPAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468	100.0	461	1 US-08-385-229-2	Sequence 2, Appli
2	2468	100.0	461	2 US-08-650-000-2	Sequence 2, Appli
3	2468	100.0	461	4 US-08-477-347-3	Sequence 3, Appli
4	2468	100.0	461	4 US-08-476-862-2	Sequence 2, Appli
5	2468	100.0	461	6 5395760-2	Patent No. 5395760
6	2462	99.8	461	4 US-09-042-785A-7	Sequence 7, Appli
7	2462	99.8	461	4 US-09-006-353A-4	Sequence 4, Appli
8	1512	61.3	474	2 US-08-650-000-4	Sequence 4, Appli
9	1512	61.3	474	4 US-09-042-785A-8	Sequence 8, Appli
10	1512	61.3	474	6 5395760-4	Patent No. 5395760
11	1433	58.1	518	1 US-08-385-229-4	Sequence 4, Appli
12	1404	56.9	486	1 US-08-243-010-1	Sequence 1, Appli
13	1312	53.2	235	3 US-09-326-394-4	Sequence 4, Appli
14	1263	51.2	227	3 US-08-974-022-48	Sequence 48, Appli
15	1263	51.2	227	4 US-08-795-445A-48	Sequence 48, Appli
16	1263	51.2	227	4 US-08-795-447A-48	Sequence 48, Appli
17	1263	51.2	227	4 US-08-974-186-48	Sequence 48, Appli
18	1263	51.2	227	4 US-08-795-446B-48	Sequence 48, Appli
19	931	37.7	163	2 US-08-219-237B-5	Sequence 5, Appli
20	931	37.7	163	4 US-08-477-347-13	Sequence 13, Appli
21	931	37.7	163	4 US-08-476-862-4	Sequence 4, Appli
22	931	37.7	163	4 US-08-468-560C-5	Sequence 5, Appli
23	924.5	37.5	164	2 US-08-232-087A-9	Sequence 9, Appli
24	695	28.2	120	3 US-08-974-022-42	Sequence 42, Appli
25	695	28.2	120	4 US-08-795-445A-42	Sequence 42, Appli
26	695	28.2	120	4 US-08-795-447A-42	Sequence 42, Appli
27	695	28.2	120	4 US-08-974-186-42	Sequence 42, Appli

28	695	28.2	120	4	US-08-795-446B-42	Sequence 42, Appli
29	453	18.4	77	4	US-08-866-545-2	Sequence 2, Appli
30	379.5	15.4	349	4	US-09-006-353A-13	Sequence 13, Appli
31	373	15.1	355	1	US-08-292-549-6	Sequence 6, Appli
32	373	15.1	355	4	US-09-006-353A-14	Sequence 14, Appli
33	360.5	14.6	326	1	US-08-292-549-4	Sequence 4, Appli
34	360.5	14.6	326	5	PCT-US91-02207-4	Sequence 4, Appli
35	351.5	14.2	300	2	US-08-794-796-2	Sequence 2, Appli
36	343.5	13.9	605	4	US-09-042-785A-23	Sequence 23, Appli
37	343.5	13.9	655	3	US-08-959-382-2	Sequence 2, Appli
38	342	13.9	299	4	US-09-286-529-17	Sequence 17, Appli
39	340	13.8	211	4	US-09-386-529-20	Sequence 20, Appli
40	330	13.4	401	3	US-08-974-022-6	Sequence 6, Appli
41	330	13.4	401	4	US-09-042-785A-12	Sequence 12, Appli
42	330	13.4	401	4	US-08-795-445A-6	Sequence 6, Appli
43	330	13.4	401	4	US-08-795-447A-6	Sequence 6, Appli
44	330	13.4	401	4	US-08-974-186-6	Sequence 6, Appli
45	330	13.4	401	4	US-08-795-446B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-385-229-2
; Sequence 2, Application US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-385-229-2

Query Match 100.0%; Score 2468; DB 1; Length 461;
Best Local Similarity 100.0%; Pred.No. 4.2e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRRLREYDQTAQMCCSKSPG 60

Db 1 MAPVAVMAALAVGLLELWAAHALPAQVAFTPYAPPEPGSTCRLREYDQTAQMCCSKCSPG 60
Qy 61 QHAKVFCTKTSDTVCDSCEDSTYTQLNWVPECLSCGSRSSDOVETQACTREONRICTC 120
Db 61 QHAKVFCTKTSDTVCDSCEDSTYTQLNWVPECLSCGSRSSDOVETQACTREONRICTC 120
Qy 121 RPYGMYCALSKEGRCRLCAPLRCRPGFVGARPGTETSDVVKCPKCAPGTFSTTSTDICR 180
Db 121 RPYGMYCALSKEGRCRLCAPLRCRPGFVGARPGTETSDVVKCPKCAPGTFSTTSTDICR 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
Db 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
Qy 241 FLPLPMGSPPAEGSTGDFALPVGLIVGTALGLLIIGVWNCVIMTVQVKKPLCLQREAKV 300
Db 241 FLPLPMGSPPAEGSTGDFALPVGLIVGTALGLLIIGVWNCVIMTVQVKKPLCLQREAKV 300
Qy 301 PHLPADKARGTQGPQOHLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
Db 301 PHLPADKARGTQGPQOHLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
Qy 361 ARASTGSSDSPGGHGTQVNVTCIVNVCSSDSSDSSQSSQASSTMGDTDSSPSPKDEQ 420
Db 361 ARASTGSSDSPGGHGTQVNVTCIVNVCSSDSSDSSQSSQASSTMGDTDSSPSPKDEQ 420
Qy 421 VPFKSKECAFRSQLETPETLLGSTEERKPLPLGVDPAGMKPS 461
Db 421 VPFKSKECAFRSQLETPETLLGSTEERKPLPLGVDPAGMKPS 461

RESULT 2

US-08-650-000-2
; Sequence 2, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,000
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,453
; FILING DATE:
; APPLICATION NUMBER: US/08/038,765
; FILING DATE:
; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,635

; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-650-000-2

Query Match 100.0%; Score 2468; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.2e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPVAVMAALAVGLLELWAAHALPAQVAFTPYAPPEPGSTCRLREYDQTAQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLLELWAAHALPAQVAFTPYAPPEPGSTCRLREYDQTAQMCCSKCSPG 60
Qy 61 QHAKVFCTKTSDTVCDSCEDSTYTQLNWVPECLSCGSRSSDOVETQACTREONRICTC 120
Db 61 QHAKVFCTKTSDTVCDSCEDSTYTQLNWVPECLSCGSRSSDOVETQACTREONRICTC 120
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Db 121 RPYGMYCALSKEGRCRLCAPLRCRPGFVGARPGTETSDVVKCPKCAPGTFSTTSTDICR 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
Db 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
Qy 241 FLPLPMGSPPAEGSTGDFALPVGLIVGTALGLLIIGVWNCVIMTVQVKKPLCLQREAKV 300
Db 241 FLPLPMGSPPAEGSTGDFALPVGLIVGTALGLLIIGVWNCVIMTVQVKKPLCLQREAKV 300
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Db 301 PHLPADKARGTQGPQOHLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
Qy 361 ARASTGSSDSPGGHGTQVNVTCIVNVCSSDSSDSSQSSQASSTMGDTDSSPSPKDEQ 420
Db 361 ARASTGSSDSPGGHGTQVNVTCIVNVCSSDSSDSSQSSQASSTMGDTDSSPSPKDEQ 420
Qy 421 VPFKSKECAFRSQLETPETLLGSTEERKPLPLGVDPAGMKPS 461
Db 421 VPFKSKECAFRSQLETPETLLGSTEERKPLPLGVDPAGMKPS 461

RESULT 3

US-08-477-347-3
; Sequence 3, Application US/08477347
; Patent No. 623246
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:

APPLICANT: WALLACH, David
 APPLICANT: BIGDA, Jacek
 APPLICANT: BELETSKY, Igor
 APPLICANT: METT, Igor
 APPLICANT: ENGELMANN, Hartmut
 TITLE OF INVENTION: TNF INHIBITORS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476.862
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IL 107267
 FILING DATE: 12-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IL 94039
 FILING DATE: 06-APR-1990

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> APPLICATION NUMBER: IL 90339
> FILING DATE: 06-AUG-1989
>
> PRIORITY APPLICATION DATA:
> APPLICATION NUMBER: IL 90339
> FILING DATE: 18-MAY-1989
> ATTORNEY/AGENT INFORMATION:
> NAME: BROWDY, Roger L.
> REGISTRATION NUMBER: 25,618
> REFERENCE/DOCKET NUMBER: WALLACH=12A
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 202-628-5197
> TELEFAX: 202-737-3528
> INFORMATION FOR SEQ ID NO: 2:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 461 amino acids
> TYPE: amino acid
> TOPOLOGY: linear
> MOLECULE TYPE: protein
>
> US-08-476-862-2

```

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;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-862-2

Query Match 100.0%; Score 2468; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.2e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 MAPVAVMAALAVGLWAAHAHALPAQVAFTPYAPEPGSTCLRLEYDQTAAQMCCSKCSGP 60
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Db 61 QHAKVFCTKTSDFVCDSCEDSTVTQLNNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
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Db 241 FLPMGSPSPAEGSTGDFALPVGLIVGTALGLLIIGVNVCIWTVKKKPLCLQREAKV 300
QY 301 PHLPADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360
Db 301 PHLPADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360
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Db 361 ARASTSSDSSPGGHGTQVNVTCIVNVCSDDHSSQCSOASSTMGDTDSSPSPKDEQ 420
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Db 421 VPFSKEECAFRSOLETPETLLGSTEKPLPLGVDPDAGMKPS 461

RESULT 5
5395760-2
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:2:
; LENGTH: 461
5395760-2

Query Match 100.0%; Score 2468; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.2e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLREYDQTAQMCCSKSPG 60
Db 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLREYDQTAQMCCSKSPG 60

QY 61 QHAKVFCTKTSDTVDCSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTC 120
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Db 121 RPYWCALSKQEGCRLCAPLRCRPGFVARPGTETSDVVKCPACPTFSNTTSSDIDICR 180

QY 181 PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240
Db 181 PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240

QY 241 FLPMGSPSPAEGSTGDFALPVGLIVGTALGLLIIGVNVCIWTVKKKPLCLQREAKV 300
Db 241 FLPMGSPSPAEGSTGDFALPVGLIVGTALGLLIIGVNVCIWTVKKKPLCLQREAKV 300

QY 301 PHLPADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360
Db 301 PHLPADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360

QY 361 ARASTSSDSSPGGHGTQVNVTCIVNVCSDDHSSQCSOASSTMGDTDSSPSPKDEQ 420
Db 361 ARASTSSDSSPGGHGTQVNVTCIVNVCSDDHSSQCSOASSTMGDTDSSPSPKDEQ 420

QY 421 VPFSKEECAFRSOLETPETLLGSTEKPLPLGVDPDAGMKPS 461
Db 421 VPFSKEECAFRSOLETPETLLGSTEKPLPLGVDPDAGMKPS 461

RESULT 6
US-09-042-785A-7
; Sequence 7, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400.
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-7

Query Match 99.8%; Score 2462; DB 4; Length 461;
Best Local Similarity 99.8%; Pred. No. 1.2e-172;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLREYDQTAQMCCSKSPG 60
Db 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLREYDQTAQMCCSKSPG 60

QY 61 QHAKVFCTKTSDTVDCSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDTVDCSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTC 120

QY 121 RPYWCALSKQEGCRLCAPLRCRPGFVARPGTETSDVVKCPACPTFSNTTSSDIDICR 180
Db 121 RPYWCALSKQEGCRLCAPLRCRPGFVARPGTETSDVVKCPACPTFSNTTSSDIDICR 180

QY 181 PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240
Db 181 PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240

QY 241 FLPMGSPSPAEGSTGDFALPVGLIVGTALGLLIIGVNVCIWTVKKKPLCLQREAKV 300
Db 241 FLPMGSPSPAEGSTGDFALPVGLIVGTALGLLIIGVNVCIWTVKKKPLCLQREAKV 300

QY 301 PHLPADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360
Db 301 PHLPADKARGTQGEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360

QY	361	* ARASTCSSDSSPGHGHTQNVNTCI	VNVCSSSHSSQSSQAASSTMGDTDS	SPSPKDEQ	420
Db	361	ARASTCSSDSSPGHGHTQNVNTCI	VNVCSSSHSSQSSQAASSTMGDTDS	SPSPKDEQ	420
QY	421	VPSKECAFRSOLETPETLLGSTE	KPLPLGVDPDAGMKPS	461	
Db	421	VPSKECAFRSOLETPETLLGSTE	KPLPLGVDPDAGMKPS	461	
RESULT 7					
US-09-006-353A-4					
; Sequence 4, Application US/09006353A					
; Patent No. 6261801					
; GENERAL INFORMATION:					
; APPLICANT: WEL, YING-FEI					
; APPLICANT: YU, GUO-LIANG					
; APPLICANT: GENTZ, REINER					
; APPLICANT: RUBEN, STEVEN					
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5					
; NUMBER OF SEQUENCES: 26					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.					
; STREET: 9410 KEY WEST AVENUE					
; CITY: ROCKVILLE					
; STATE: MD					
; COUNTRY: US					
; ZIP: 20850					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/09/006,353A					
; FILING DATE:					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: BROOKES, ANDERS A					
; REGISTRATION NUMBER: 36,373					
; REFERENCE/DOCKET NUMBER: PF341					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (301) 309-8504					
; TELEFAX: (301) 309-8512					
; INFORMATION FOR SEQ ID NO: 4:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 461 amino acids					
; TYPE: amino acid					
; STRANDEDNESS: single					
; TOPOLOGY: linear					
; MOLECULE TYPE: protein					
US-09-006-353A-4					
Query Match 99.8%; Score 2462; DB 4; Length 461;					
Best Local Similarity 99.8%; Pred. No. 1.2e-172;					
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps					
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Db	1	MAPVAVMAALAVGLELWAAHAALPAQVATTPA	PEPGSTCRLREYYDQTAQMCCSKSPG	60	
QY	61	QHAKVCTKTSDFVCDSCEDSTVTQLWNWVPECL	SGRCSSDQVETQACTREQNRICTC	120	
Db	61	QHAKVCTKTSDFVCDSCEDSTVTQLWNWVPECL	SGRCSSDQVETQACTREQNRICTC	120	
QY	121	RPGWYCALSKQECRCRLCAPLKRCPFGFVARPCGTETSDVVCKP	CAFGTETSDVTSSTDICR	180	
Db	121	RPGWYCALSKQECRCRLCAPLKRCPFGFVARPCGTETSDVVCKP	CAFGTETSDVTSSTDICR	180	
QY	181	PHOICNVVAIPGNASMDVACTSTPTRSNAPAGVHLHPQVSTRSOHTQ	TPTPEPSTAPSTS	240	
Db	181	PHOICNVVAIPGNASMDVACTSTPTRSNAPAGVHLHPQVSTRSOHTQ	TPTPEPSTAPSTS	240	

US-08-650-000-4

Query Match 61.3%; Score 1512; DB 2; Length 474;
Best Local Similarity 63.0%; Pred. No. 3.8e-103;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

QY 1 MAPVAVAAALVAGLELWAAAHALPAQVAFTPYAPPEPGSTCRL-REYDQTAQMCCKSCSP 59
DB 1 MAPAALWVAVFELQWATHTVPAQVLTTPYKPEPGYECQISQEYDRAQMCCKACPP 60
QY 60 GQAKVFCSTKTDVCDSCEDSTYTQLNWVPECLSCGSRCSDDQVETQACTREQNRIC 119
DB 61 GQVVKHFCNKTSITVADCEASMYTQVWQFRTCLSCSSCTTDDQVEIRACTKQONRVCA 120
QY 120 CRPGWCALSKQEG-CRLCAPLRCRPGFGVARGPTETSDVCKPCAPGTFSTNTSSTD 178
DB 121 CEAGRYCALKTHSGRCQCMRLSKGPGFGVASSRAPNGVLCACAPGTFSDTTSSTDV 180
QY 179 CRPHQICNVVAIPGNASMDAVCTSTPTSRMAPCAVHLPOPVSTRSQHTOPTPEPSTAPS 238
DB 181 CRPHRICSLAIPGNASTDAVCAPESTLSAIPRTLVVSQPEPTRSQPLDQEPGQSOTP- 239
QY 239 TSFLLPMGSPPPAEGST-GDFALPVGLIVGTALGLLIIGVWNCVIMTQVKKKPLCLQRE 297
DB 240 -SILTSLSGSPPIEQSTKGGISLPIGLIVGTSLGLMLGLVNCIILVQRKKKPSCLQRD 298
QY 298 AKVPHLPADKARGTQGPQOQHLLITAPSSSSSLESSASALDRAPTRNQPAPGV-EAS 356
DB 299 AKVPHVPDEKSDQAVGLEQQHLLITAPSSSSSLESSASAGDRRAPPGHPPQARVMAEQ 358
QY 357 GAGEARASTGSSDPGGHGTQVNVTCIVNVCSSSDHSSCSOASSTMGDTSSPSESP 416
DB 359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSCSOASATVGDPAKPRASP 418
QY 417 KDEQVPFSKECAFRRSQLETPTLLGSTEKPLPLGVDPDAGMKPS 461
DB 419 KDEQVPFSQECPSQSPCETTEL--QSHEKPLPLGVDPDGMKPS.461

RESULT 9
US-09-042-785A-8
Sequence 8, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-8

Query Match 61.3%; Score 1512; DB 4; Length 474;
Best Local Similarity 63.0%; Pred. No. 3.8e-103;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

QY 1 MAPVAVAAALVAGLELWAAAHALPAQVAFTPYAPPEPGSTCRL-REYDQTAQMCCKSCSP 59
DB 1 MAPAALWVAVFELQWATHTVPAQVLTTPYKPEPGYECQISQEYDRAQMCCKACPP 60
QY 60 GQAKVFCSTKTDVCDSCEDSTYTQLNWVPECLSCGSRCSDDQVETQACTREQNRIC 119
DB 61 GQVVKHFCNKTSITVADCEASMYTQVWQFRTCLSCSSCTTDDQVEIRACTKQONRVCA 120
QY 120 CRPGWCALSKQEG-CRLCAPLRCRPGFGVARGPTETSDVCKPCAPGTFSTNTSSTD 178
DB 121 CEAGRYCALKTHSGRCQCMRLSKGPGFGVASSRAPNGVLCACAPGTFSDTTSSTDV 180
QY 179 CRPHQICNVVAIPGNASMDAVCTSTPTSRMAPCAVHLPOPVSTRSQHTOPTPEPSTAPS 238
DB 181 CRPHRICSLAIPGNASTDAVCAPESTLSAIPRTLVVSQPEPTRSQPLDQEPGQSOTP- 239
QY 239 TSFLLPMGSPPPAEGST-GDFALPVGLIVGTALGLLIIGVWNCVIMTQVKKKPLCLQRE 297
DB 240 -SILTSLSGSPPIEQSTKGGISLPIGLIVGTSLGLMLGLVNCIILVQRKKKPSCLQRD 298
QY 298 AKVPHLPADKARGTQGPQOQHLLITAPSSSSSLESSASALDRAPTRNQPAPGV-EAS 356
DB 299 AKVPHVPDEKSDQAVGLEQQHLLITAPSSSSSLESSASAGDRRAPPGHPPQARVMAEQ 358
QY 357 GAGEARASTGSSDPGGHGTQVNVTCIVNVCSSSDHSSCSOASSTMGDTSSPSESP 416
DB 359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSCSOASATVGDPAKPRASP 418
QY 417 KDEQVPFSKECAFRRSQLETPTLLGSTEKPLPLGVDPDAGMKPS 461
DB 419 KDEQVPFSQECPSQSPCETTEL--QSHEKPLPLGVDPDGMKPS 461

RESULT 10
5395760-4
Patent No. 5395760
APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO:4
LENGTH: 474
5395760-4

Query Match 61.3%; Score 1512; DB 6; Length 474;
Best Local Similarity 63.0%; Pred. No. 3.8e-103;

Matches	293	Conservative	50	Mismatches	114	Indels	8	Gaps
Qy	1	MAPVAVNAALAVGLIELMAAAHALPAQVAFTPYAPPGSTCRL-REYYDQTAMCCSKSCP	59					
Db	1	MAPAALVAVLFEQLMAGTGTVAQVVLTPYKPEPGYECQISQEVYDRKAQMCCAKCP	60					
Qy	60	GOHAKVFCTKTSDTVDCSDCESTVYTLQNNWPECLSCGSRCSDDQVETACATREONRICT	119					
Db	61	GOYVKHFCNKTSDTVACDCEASWYTVQWVQFTCLSCSSCSTTDQVEIRACTKQQRNCA	120					
Qy	120	CRPGWCALSKQEG-CRLCAPLKRCPGFGVARPGTETSDVYCKPCAPGTFNTTSTSDI	178					
Db	121	CEAGRYCALKTHSGCROCMRLSKCGPGFVASSRAPNGNLVCKACAPGTFSDTTSSTDV	180					
Qy	179	CRPHOICNNVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVYSTRSQHTPPTPEPSTPS	238					
Db	181	CRPHRICSLAIPGNASTDAVCAPESPSTLSAIPRTLYVSQPEPTRSQDQDEPGPSQTP-	239					
Qy	239	TSFLPLMGPSPPAEGST-GDFALPGLVIGVTALGLLIIGVYVNCVIMTQVKKKPLCLQRE	297					
Db	240	-SILTSLSGTPIEQSTKGGISLPIGLIVGTSILGLMLGLVNCIILVQRKKKPSCLQRD	298					
Qy	298	AKVPHLLADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRAPTRNQOPAGV-EAS	356					
Db	299	AKVPHVVPDEKSQDAVGLQOQHLLITAPSSSSSSLESSASAGDRAPPGGHPQARVMAEQ	358					
Qy	357	GAGEARASTGSDSSPGGHGTQVNVTCIVNVCCSSDHSQCSQASSTMGDTDSSPESP	416					
Db	359	GFQEARASSRISDSSHGSHGTHVNVTCIVNVCCSSDHSQCSQASATVGDGPAKFSAP	418					
Qy	417	KDEOVPSFKBCAPRSQLETPETTLGGSTEEKPLPLGVDPDAGMKPS	461					
Db	419	KDEOVPSFQECPSQSPQETTEL--QSHKXPPLPLGVDPDMGKPS	461					

RESULT 11
US-08-385-229-4
; Sequence 4, Application US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 518 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-385-229-4

Query Match          59.1%; Score 1433; DB 1; Length 518;
Best Local Similarity 64.5%; Pred. No. 2.5e-97;
Matches 289; Conservative 22; Mismatches 67; Indels 7

Qy 1 MAPVAVMAALAVGLLEWAAAHALPAQVAFTPYAPBPGSTCRLREYYDOTAQMCSCS
Db 30 MAPVAVMAALAVGLLEWAAAHALPAQVAFTPYAPBPGSTCRLREYYDOTAQMCSCS
Qy 61 QHAKVFCTKTSDDTVCDSCSEDSTYTLQNNWVPECLSCGSCSSDDVETQACTREQ
Db 90 QHAKVFCTKTSDDTVCDSCSEDSTYTLQNNWVPECLSCGSCSSDDVETQACTREQ
Qy 121 RPYGWCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVWCKPCAPGTFSSNTTS
Db 150 RPYGWCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVWCKPCAPGTFSSNTTS
Qy 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPCAVHLPOPVSTRSQHTQPTPEPST
Db 210 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPCAVHLPOPVSTRSQHTQPTPEPST
Qy 241 FLLPMGPPRAEGSGDGFALPGLVIGTVLGLLLIIGVNVVIMQVKKKKPLCLQL
Db 270 FLLPMGPPRAEGSGTGD-----
Qy 301 PHLPADKARGTQGPQEQHLLITAPSSSSSSSSASALDRRAP-----TRN
Db 298 PCCPAPELLG--GPS-----VLFPPKPKDLMIS-----RTPEVTCVVVDVSH
Qy 350 ----APGVASGAGEARASTGSDSPSGHGHTQNVVTCIVNV--CSSSDHSQSCS
Db 346 FNIWYDGVGEVH-----NAKTPREEQYNSTRVYVSVLTVLHQDWLNGDKYCKYK
Qy 403 STMGDTSDSPSPKDEQV---PFSKEE 427
Db 401 APMQKTIISKAKGPQEPQVYTLPPSRDE 428

RESULT 12
US-08-243-010-1
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lauffer, Leander
; APPLICANT: Zettlmeissel, Gerd
; APPLICANT: Quendo, Patricia
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/798,564
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: DE P 40 37 837.3
; FILING DATE: 28-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1132-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 486 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-243-010-1

Query Match          56.9%; Score 1404; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 3.1e-95;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPGPGSTCRLREYYDQTQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPGPGSTCRLREYYDQTQMCCSKCSPG 60
QY 61 QHAKVFCTKTSDIVDCSDSTYTLNWNVPECLSCGSRSSDQVETQACTREONRICTC 120
Db 61 QHAKVFCTKTSDIVDCSDSTYTLNWNVPECLSCGSRSSDQVETQACTREONRICTC 120
QY 121 RPYWCYCALSKOEGCRLCAPLKRCPGFGVAPGPGTETSDVVCKPCAPGTFSTSTDCR 180
Db 121 RPYWCYCALSKOEGCRLCAPLKRCPGFGVAPGPGTETSDVVCKPCAPGTFSTSTDCR 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 240
Db 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 240
QY 241 FILPMGSPPAE 252
Db 241 FILPMGSPPAE 252

RESULT 13
US-09-326-394-4
; Sequence 4, Application US/09326394
; Patent No. 6306820
; GENERAL INFORMATION:
; APPLICANT: Bendele, Alison M.
; APPLICANT: Sennello, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/326,394
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 60/032,587
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zindrick, Thomas K.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-326-394-4

Query Match          53.2%; Score 1312; DB 4; Length 235;
Best Local Similarity 99.6%; Pred. No. 6.8e-89;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LPAQVAFTPYAPGPGSTCRLREYYDQTQMCCSKCSPGQHAKVFCTKTSDIVDCSDST 82
Db 1 LPAQVAFTPYAPGPGSTCRLREYYDQTQMCCSKCSPGQHAKVFCTKTSDIVDCSDST 60
QY 83 YTQLNWNVPECLSCGSRSSDQVETQACTREONRICTCRPGWYCALSKOEGCRLCAPLKR 142
Db 61 YTQLNWNVPECLSCGSRSSDQVETQACTREONRICTCRPGWYCALSKOEGCRLCAPLKR 120
QY 143 CRPGFGVAPGPGTETSDVVCKPCAPGTFSTSTDCRPHQICNVVAIPGNASMDAVCTS 202
Db 121 CRPGFGVAPGPGTETSDVVCKPCAPGTFSTSTDCRPHQICNVVAIPGNASMDAVCTS 180
QY 203 TSPTSRMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSFLPMGSPPAEGSTGD 257
Db 181 TSPTSRMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSFLPMGSPPAEGSTGD 235

RESULT 14
US-08-974-022-48
; Sequence 48, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-48

Query Match 51.2%; Score 1263; DB 3; Length 227;
Best Local Similarity 99.6%; Pred. No. 2.5e-85;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
DB 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
QY 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
DB 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
QY 121 RPGWCALSKQEGCRLCAPLRKCPGFGVARPGTETSDVVKPCAPGTFSTNTSSSTDICR 180
DB 121 RPGWCALSKQEGCRLCAPLRKCPGFGVARPGTETSDVVKPCAPGTFSTNTSSSTDICR 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227
DB 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227

RESULT 15

US-08-795-445A-48
Sequence 48, Application US/08795445A
Patent No. 6284485

GENERAL INFORMATION:

APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 Behavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 227 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-48

Query Match 51.2%; Score 1263; DB 4; Length 227;
Best Local Similarity 99.6%; Pred. No. 2.5e-85;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
DB 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
QY 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
DB 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
QY 121 RPGWCALSKQEGCRLCAPLRKCPGFGVARPGTETSDVVKPCAPGTFSTNTSSSTDICR 180
DB 121 RPGWCALSKQEGCRLCAPLRKCPGFGVARPGTETSDVVKPCAPGTFSTNTSSSTDICR 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227
DB 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227

Search completed: February 12, 2002, 12:48:00
Job time: 152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: February 12, 2002, 13:02:20 ; Search time 12.79 seconds
(without alignments)
136.983 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_185

Perfect score: 134

Sequence: 1 PCAPGTFSTSTSDICRPHQIC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4466

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	23.1	20	A42865	Ca2+/calmodulin-de
2	30	22.4	18	B49048	T-cell receptor be
3	29	21.6	13	S47381	T-cell antigen rec
4	29	21.6	16	S38292	30K allergen - rye
5	29	21.6	17	A60317	glucagon-like pept
6	29	21.6	21	I54351	gene HEXA protein
7	29	21.6	22	A39269	Lx-1 tumor antigen
8	28	20.9	23	S60565	homeodomain protei
9	27	20.1	20	T48881	leader peptide [im
10	27	20.1	22	1 MKN1	mu-conotoxin GIIIA
11	26	19.4	15	JN0263	antigen (clone PVI
12	26	19.4	16	B60278	24K antigen - Myco
13	26	19.4	20	I54283	arylsulfatase A -
14	26	19.4	23	A59048	convulsant peptide
15	25.5	19.0	22	I37144	aspartylglycosamin
16	25.5	19.0	23	E39855	paralytic peptide
17	25.5	19.0	23	D39855	paralytic peptide
18	25	18.7	11	S23308	substance P - rain
19	25	18.7	13	P00491	self-incompatibili
20	25	18.7	13	D56661	S-locus specific g
21	25	18.7	17	B61334	trypsin (EC 3.4.21
22	25	18.7	19	B56613	virion morphogenes
23	25	18.7	19	C56661	S-locus specific q
24	25	18.7	19	P00492	self-incompatibili
25	25	18.7	22	1 MKN2	mu-conotoxin GIIIB
26	25	18.7	22	1 MKN3	mu-conotoxin GIIIC
27	25	18.7	23	A48968	exo-poly-alpha-gal
28	25	18.7	23	B38671	peptidylglycine mo
29	24	17.9	11	PH0891	T-cell receptor be

30 24 17.9 14 2 PH0776 T-cell receptor al
31 24 17.9 19 2 A05305 hemoglobin beta-2
32 24 17.9 21 2 C39543 collagen alpha 3(I
33 23.5 17.5 16 2 B54877 alpha-conotoxin Ph
34 23.5 17.5 20 2 A34859 heliothermine - Mex
35 23.5 17.5 23 2 F39855 paralytic peptide
36 23.5 17.5 23 2 G39855 paralytic peptide
37 23 17.2 12 1 JTJGO tremmerogen A-10 -
38 23 17.2 12 2 I40663 bma protein - Cios
39 23 17.2 13 2 G22565 R-phycoerythrin ga
40 23 17.2 13 2 PS0453 36K protein 3124 -
41 23 17.2 13 2 PH0799 T-cell receptor al
42 23 17.2 14 2 B61309 lutropin beta chai
43 23 17.2 15 2 A49155 vasotocin-associat
44 23 17.2 15 2 PH0782 T-cell receptor al
45 23 17.2 16 2 PH1634 Ig H chain V-D-J r

ALIGNMENTS

RESULT 1
A42865
Ca2+/calmodulin-dependent myosin light chain kinase (autophosphorylation sites) - rab
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: A42865
R:Gao, Z.H.; Moomaw, C.R.; Hsu, J.; Slaughter, C.A.; Stull, J.T.
Biochemistry 31, 6126-6133, 1992
A:Title: Autophosphorylation of skeletal muscle myosin light chain kinase.
A:Reference number: A42865; MUID:92329432
A:Accession: A42865
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GAO>
A:Experimental source: skeletal muscle
A:Note: sequence extracted from NCBI backbone (NCBIP:109204)
C:Keywords: calmodulin binding

Query Match 23.1% Score 31; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 9;

QY 3 APGTFSTSTSDICR 18
Db 2 APGQADQAKAGDTCR 17
||| : |||
||| : |||

RESULT 2
B49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (Fragmen
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: B49048
R:Sloud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
A:Reference number: A49048; MUID:92387250
A:Accession: B49048
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-18 <STO>
A:Experimental source: patient EV, IL-2R+ synovial T-cells
A:Note: sequence extracted from NCBI backbone (NCBIP:113264)
C:Keywords: T-cell receptor

Query Match 22.4% Score 30; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 4;

QY 2 CAPGTFSTNT 11

Db 7 CAPGXYGYT 16
||||| : |

RESULT 3

S47381

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47381

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47381

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: EMBL:Z35698; NID:g527487; PIDN:CAA84767.1; PID:g527488

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 21.6%; Score 29; DB 2; Length 13;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAPGTFPSNT 10

Db 1 CASSTRSNPT 9

RESULT 4

S38292

30K allergen - rye (fragment)

C:Species: Secale cereale (rye)

C>Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 07-May-1999

C:Accession: S38292

R:Peterson, A.; Schramm, G.; Becker, W.M.; Schlaak, M.

Biol. Chem. Hoppe-Seyler 374, 855-861, 1993

A:Title: Comparison of four grass pollen species concerning their allergens of grass

A:Reference number: S38288; MUID:94092339

A:Accession: S38292

A:Molecule type: protein

A:Residues: 1-16 <PET>

Query Match

Best Local Similarity 21.6%; Score 29; DB 2; Length 16;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PCAPGT 6

Db 7 PAAPGT 12

RESULT 5

A60317

glucagon-like peptide 1 - marbled electric ray (fragment)

C:Species: Torpedo marmorata (marbled electric ray)

C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 21-Nov-1997

C:Accession: A60317

R:Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.

Regul. Pept. 13, 94, 1986

A:Title: A truncated glucagon-like peptide I from torpedo pancreas.

A:Reference number: A60317

A:Accession: A60317

A:Molecule type: protein

A:Residues: 1-17 <CON>

C:Superfamily: glucagon

C:Keywords: duplication; pancreas

Query Match

Best Local Similarity 21.6%; Score 29; DB 2; Length 17;

Best Local Similarity 38.5%; Pred. No. 7.7e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 APGTFSTSTSD 15

Db 2 AEGTYTSDVSSLB 14

RESULT 6

I54351

gene HEXA protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I54351

R:Akli, S.; Chomel, J.C.; Lacorte, J.M.; Bachner, L.; Poenaru, L.

Hum. Mol. Genet. 2, 61-67, 1993

A:Title: Ten novel mutations in the HEXA gene in non-Jewish Tay-Sachs patients.

A:Reference number: I54351; MUID:93258352

A:Accession: I54351

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-21 <RES>

A:Cross-references: GB:S61298; NID:g300412; PIDN:AAD13927.1; PID:g4261627

C:Genetics:

A:Gene: GDB:HEXA

A:Cross-references: GDB:I20040; OMIM:272800

A:Map position: 15q23-15q24

C:Superfamily: beta-hexosaminidase

Query Match

Best Local Similarity 21.6%; Score 29; DB 2; Length 21;

Matches 10; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

Qy 5 GT-PSNTSTSDICR-PHQ 21

Db 1 GTFFINKTEIEDFRFPHQ 19

RESULT 7

A39269

LX-1 tumor antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 05-Jan-1996

C:Accession: A39269

R:Rosenbaum, L.C.; Newwelt, E.A.; Van Tol, H.H.M.; Loh, Y.P.; Verbalis, J.G.; Hellstr

Proc. Natl. Acad. Sci. U.S.A. 87, 9928-9932, 1990

A:Title: Expression of neurophysin-related precursor in cell membranes of a small-cel

A:Reference number: A39269; MUID:91088624

A:Accession: A39269

A:Molecule type: protein

A:Residues: 1-22 <ROS>

C:Superfamily: oxytocin-neurophysin

Query Match

Best Local Similarity 21.6%; Score 29; DB 2; Length 22;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PCAPG 5

Db 12 PCGPG 16

RESULT 8

S60565

homeodomain protein hrox3 - California red abalone (fragment)

C:Species: Haliotis rufescens (California red abalone)

C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999

C:Accession: S60565

R:Begnan, B.M.; Morse, D.E.

Mol. Marine Biol. Biotechnol. 2, 1-9, 1993

A:Title: Identification of eight homeobox-containing transcripts expressed during lar

A:Reference number: S60564; MUID:93372986

A:Accession: S60565

A:Molecule type: mRNA

A:Residues: 1-23 <DE>

A:Cross-references: EMBL:X79372; NID:9495110; PIDN:CAA55917.1; PID:9495111

C:Genetics:

A:Gene: hrox3

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 20.9%; Score 28; DB 2; Length 23;

Best Local Similarity 57.1%; Pred. No. 1.4e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 16 ICRPHQI 22

||| :|

Db 5 LCRPRRI 11

RESULT 9

T48881

leader peptide [Imported] - Vibrio sp.

C:Species: Vibrio sp.

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T48881

R:Xu, Y.; Zhang, Y.; Liang, Z.Y.; Van de Casteele, M.; Legrain, C.; Glansdorff, N.

Microbiology 144, 1435-1441, 1998

A:Title: Aspartate carbamoyltransferase from a psychrophilic deep-sea bacterium, *Vibrio*

A:Reference number: 224845

A:Accession: T48881

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-20 <XUY>

A:Cross-references: EMBL:Y09786; PIDN:CAA70922.1

A:Experimental source: strain 2693

Query Match 20.1%; Score 27; DB 2; Length 20;

Best Local Similarity 41.7%; Pred. No. 1.7e+03;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 9 NTTSTDCRPH 20

::| :|||

Db 7 SSLSSFKLVPRH 18

RESULT 10

MXKNI

mu-conotoxin GIIA [validated] - cone shell (*Conus geographus*)

N:Alternate names: geographotoxin I (GTx I); myotoxin I

C:Species: *Conus geographus* (geography cone)

C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 15-Sep-2000

C:Accession: A01786; A23579

R:Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.

FEBS Lett. 155, 277-280, 1983

A:Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins from

A:Reference number: A91309; MUID:83210170

A:Accession: A01786

A:Molecule type: protein

A:Residues: 1-22 <SAT>

R:Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczyld

J. Biol. Chem. 260, 9280-9288, 1985

A:Title: *Conus geographus* toxins that discriminate between neuronal and muscle sodium ch

A:Reference number: A23579; MUID:85261316

A:Accession: A23579

A:Molecule type: protein

A:Residues: 1-22 <CRU>

R:Kohda, D.; Lancelin, J.M.; Inagaki, F.; Wakamatsu, K.

submitted to the Brookhaven Protein Data Bank, December 1992

A:Reference number: A51994; PDB:1ITC

A:Contents: annotation; conformation by (1)H-NMR, residues 1-22

R:Lancelin, J.M.; Kohda, D.; Tate, S.I.; Yanagawa, Y.; Abe, T.; Satake, M.; Inagaki, F.

Biochemistry 30, 6908-6916, 1991

A:Title: Tertiary structure of conotoxin GIIA in aqueous solution.

A:Reference number: A44659; MUID:91299744

A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR

R:Ott, K.H.; Becker, S.; Gordon, R.D.; Rueterjans, H.

FEBS Lett. 278, 160-166, 1991

A:Title: Solution structure of mu-conotoxin GIIA analysed by 2D-NMR and distance geo

A:Reference number: A58581; MUID:91122275

C:Contents: annotation; conformation by (1)H-NMR

R:Wakamatsu, K.; Kohda, D.; Hatanaka, H.; Lancelin, J.M.; Ishida, Y.; Oya, M.; Nakamu

Biochemistry 31, 12577-12584, 1992

A:Title: Structure-activity relationships of mu-conotoxin GIIA: structure determinat

A:Reference number: A44244; MUID:93112598

C:Contents: annotation; conformation by (1)H-NMR

C:Superfamily: mu-conotoxin

C:Keywords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor

F:3-15,4-20,10-21/disulfide bonds: #status experimental

F:6,7/Modified site: 4-hydroxyproline (Pro) #status experimental

F:17/Modified site: 4-hydroxyproline (Pro) #status experimental

F:22/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 20.1%; Score 27; DB 1; Length 22;

Best Local Similarity 42.9%; Pred. No. 1.8e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 17 CRPHQIC 23

||| :|

Db 15 CKPQRC 21

RESULT 11

JN0263

antigen (clone PV12) - Plasmodium vivax (fragment)

C:Species: Plasmodium vivax

C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Sep-1997

C:Accession: JN0263; S21344

R:Ray, P.; Sharma, Y.D.

Biochem. Biophys. Res. Commun. 184, 668-672, 1992

A:Title: Molecular cloning and serological characterization of a new Plasmodium vivax

A:Reference number: JN0263; MUID:92246949

A:Accession: JN0263

A:Molecule type: DNA

A:Residues: 1-15 <RAY>

A:Cross-references: GB:X53681; NID:gl0084; PID:gl0085

Query Match 19.4%; Score 26; DB 2; Length 15;

Best Local Similarity 54.5%; Pred. No. 1.8e+03;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PGTFSTNTSST 14

||| :|||

Db 3 PGQHSETLVST 13

RESULT 12

B60278

24K antigen - Mycobacterium bovis (fragment)

C:Species: Mycobacterium bovis

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Jun-1993

C:Accession: B60278

R:Rifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.

Infect. Immun. 59, 800-807, 1991

A:Title: Purification and characterization of major antigens from a Mycobacterium bo

A:Reference number: A60278; MUID:91147217

A:Accession: B60278

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <FIF>

Query Match 19.4%; Score 26; DB 2; Length 16;

Best Local Similarity 38.5%; Pred. No. 1.9e+03; Mismatches 7; Indels 0; Gaps 0;

A;Residues: 1-22 <RES>
A;Cross-references: EMBL:X73071; NID:g312227; PIDN:CAA51529.1; PID:g312228
C;Genetics:
A;Gene: AGU

QY 3 APTGFSNTTSSD 15
|||
Db 1 APTTYKEELKGT 13

RESULT 13
I54283

arylsulfatase A - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I54283
R:Regis. S.; Carozzo, R.; Filocamo, M.; Serra, G.; Mastropaolo, C.; Gatti, R.
Hum. Genet. 96, 233-235, 1995
A:Title: An AT-deletion causing a frameshift in the arylsulfatase A gene of a late infant
A:Reference number: I54283; MUID:95362256
A:Accession: I54283
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:Cross-references: GB:S78735; NID:gl037139; PIDN:AAB35013.1; PID:gl037140

Query Match 19.4%; Score 26; DB 2; Length 20;

Best Local Similarity 44.4%; Pred. No. 2.3e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 TSSTDICRP 19
::: |||
Db 1 SAHSDHCRP 9

RESULT 14

A59048
convulsant peptide - cone shell (Conus textile)
C:Species: Conus textile (cloth-of-gold cone)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C:Accession: A59048
R:Cruz, L.J.; Ramilo, C.A.; Corpuz, G.P.; Olivera, B.M.
Biol. Bull. 183, 159-164, 1992
A:Title: Conus peptides: phylogenetic range of biological activity.
A:Reference number: A59048
A:Accession: A59048
A:Molecule type: protein
A:Residues: 1-23 <GRU>
C:Keywords: amidated carboxyl end; neurotoxin; venom
F:23/Modified site: amidated carboxyl end (pro) #status predicted

Query Match 19.4%; Score 26; DB 2; Length 23;

Best Local Similarity 27.8%; Pred. No. 2.6e+03; Mismatches 2; Indels 4; Gaps 1;

Matches 5; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 2 CAPGFSNTTSDICRP 19
|||
Db 9 CCPPAYCEASG---CRP 22

RESULT 15

I37144
aspartylglycosaminuria - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I37144
R:Park, H.; Vettese, M.B.; Fensom, A.H.; Fisher, K.J.; Aronson, N.N.
Biochem. J. 290, 735-741, 1993
A:Title: Characterization of three alleles causing aspartylglycosaminuria: two from a Br
A:Reference number: I37144; MUID:93207523
A:Accession: I37144
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

Query Match 19.0%; Score 25.5; DB 2; Length 22;

Best Local Similarity 38.9%; Pred. No. 2.9e+03; Mismatches 0; Indels 7; Gaps 1;

Matches 7; Conservative 0; Mismatches 4; Indels 7; Gaps 1;

QY 6 TFSNTTSTSDICRPHQIC 23
||| |
Db 5 TFSRRVS-----HHIC 15

Search completed: February 12, 2002, 13:04:11
Job time: 111 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 13:03:56 ; Search time 10.06 seconds
(without alignments)
83.826 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_185
Perfect score: 134
Sequence: 1 PCAPGTFSTSTSDICRPHQIC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1274

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	20.1	22	1 CXM1_CONGE	P01523 Conus geogr
2	27	20.1	23	1 AFP2_BRANA	P30226 brassica na
3	25.5	19.0	23	1 CF23_SPOER	P56683 spodoptera
4	25.5	19.0	23	1 PAP2_SPOEX	P30256 spodoptera
5	25.5	19.0	23	1 PAP3_SPOEX	P30257 spodoptera
6	25	18.7	11	1 TKNA_ONCMY	P28499 oncorhynch
7	25	18.7	22	1 CXM2_CONGE	P01524 Conus geogr
8	25	18.7	22	1 CXM3_CONGE	P05482 Conus geogr
9	24.5	18.3	22	1 LANM_STRMU	P80666 streptococ
10	24	17.9	19	1 HBB2_UROHA	P18992 uromastix h
11	23.5	17.5	15	1 DCMW_PSECA	P19920 pseudomonas
12	23.5	17.5	16	1 CXAB_CONPE	P50985 Conus penna
13	23.5	17.5	20	1 HELT_HELHO	P46693 helioderma h
14	23.5	17.5	23	1 PAP1_HELVI	P30251 heliothis v
15	23.5	17.5	23	1 PAP2_HELVI	P30252 heliothis v
16	23	17.2	12	1 TAI0_TREME	P01371 tremella me
17	23	17.2	15	1 CIOA_RAT	P31720 rattus norv
18	22.5	16.8	23	1 PAP2_MANSE	P30254 manduca sex
19	22	16.4	20	1 JHBP_BOMMO	P81627 bombyx mori
20	22	16.4	23	1 PAP1_SPOEX	P30255 spodoptera
21	21.5	16.0	23	1 CXAA_CONPE	P50984 Conus penna
22	21	15.7	9	1 RS11_SALTU	O54296 salmonella
23	21	15.7	15	1 NUO3_SALTU	P80263 solanum tub
24	21	15.7	18	1 CXAL_CONER	P50982 Conus ermin
25	21	15.7	20	1 PSBH_SYNVU	P19052 synechococ
26	21	15.7	22	1 SETB_SALTU	P33027 salmonella
27	21	15.7	22	1 TX12_TRIPA	P24335 trimeresur
28	20	14.9	19	1 MIFH_TRISP	P81529 trichinella
29	20	14.9	20	1 UCRO_EQUAR	P81247 equisetum a
30	20	14.9	21	1 MCT3_MOUSE	P21843 mus musculu
31	20	14.9	23	1 RL5_HALHA	P50556 halobacteri
32	19.5	14.6	15	1 DCMW_PSECH	P19917 pseudomonas
33	19.5	14.6	23	1 PAP1_MANSE	P30253 manduca sex

ALIGNMENTS

RESULT 1	CXMI_CONGE	STANDARD;	PRT;	22 AA.
ID	CXMI_CONGE	STANDARD;	PRT;	22 AA.
AC	P01523;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	MU-CONOTOXIN GIIIA (MYOTOXIN I) (GEOGRAPHUTOXIN I) (GTX-I).			
OS	Conus geographus (geography cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxID=6491;			
RN	[1]			
RN	SEQUENCE.			
RX	MEDLINE=85261316; PubMed=2410412;			
RA	Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,			
RA	Yoshikami D., Moczydlowski E.;			
RT	"Conus geographus toxins that discriminate between neuronal and			
RT	muscle sodium channels.";			
RL	J. Biol. Chem. 260:9280-9288(1985).			
RN	[2]			
RN	SEQUENCE.			
RX	MEDLINE=83210170; PubMed=6852238;			
RA	Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.;			
RT	"The amino acid sequences of homologous hydroxyproline-containing			
RT	myotoxins from the marine snail Conus geographus venom.";			
RL	FEBS Lett. 155:277-280(1983).			
RN	[3]			
RN	DISULFIDE BONDS.			
RX	MEDLINE=90249506; PubMed=2338142;			
RA	Hidaka Y., Sato K., Nakamura H., Kobayashi J., Ohizumi Y.,			
RA	Simonishi Y.;			
RT	"Disulfide pairings in geographutoxin I, a peptide neurotoxin from			
RT	Conus geographus.";			
RL	FEBS Lett. 264:29-32(1990).			
RN	[4]			
RN	REVIEW.			
RX	MEDLINE=89024586; PubMed=3052286;			
RA	Gray W.R., Olivera B.M., Cruz L.J.;			
RT	"Peptide toxins from venomous Conus snails.";			
RL	Annu. Rev. Biochem. 57:665-700(1988).			
RN	[5]			
RN	STRUCTURE BY NMR.			
RX	MEDLINE=9112275; PubMed=1991506;			
RA	Ott K.-H., Becker S., Gordon R.D., Rueterjans H.;			
RT	"Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and			
RT	distance geometry calculations.";			
RL	FEBS Lett. 278:160-166(1991).			
RN	[6]			
RN	STRUCTURE BY NMR.			
RX	MEDLINE=91299744; PubMed=2069951;			
RA	Lancelin J.-M., Kohda D., Tate S.-I., Yanagawa Y., Satake M.,			
RA	Inagaki F.;			
RT	"Tertiary structure of conotoxin GIIIA in aqueous solution.";			
RL	Biochemistry 30:6308-6316(1991).			
CC	!- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK			

CC MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
 CC CHANNELS.
 DR PIR; A01786; MXKN1.
 DR PIR; A23579; A23579.
 DR PDB; 1TCG; 31-JAN-94.
 DR PDB; 1TCH; 31-JAN-94.
 DR PDB; 1TCJ; 31-JAN-94.
 DR PDB; 1TCK; 31-JAN-94.
 KW Sodium channel inhibitor; Hydroxylation; Amidation; Venom;
 3D-structure.
 FT DISULFID 3 15
 FT DISULFID 4 20
 FT DISULFID 10 21
 FT MOD_RES 6 6
 FT MOD_RES 7 7
 FT MOD_RES 17 17
 FT MOD_RES 22 22
 FT MOD_RES 13 16
 FT HELIX 19 21
 FT TURN 19 21
 SQ SEQUENCE 22 AA; 2568 MW; F6CB02ADB359813C CRC64;

Query Match 20.1%; Score 27; DB 1; Length 22;
 Best Local Similarity 42.9%; Pred. No. 5.1e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 17 CRPHQIC 23
 I : I : I :
 DB 15 CKPQRC 21

RESULT 2
 APP2_BRANA STANDARD; PRT; 23 AA.
 AC P30226;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE CYSTEINE-RICH ANTIFUNGAL PROTEIN 2 (APP2) (FRAGMENT).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: POSSESSES ANTIFUNGAL ACTIVITY SENSITIVE TO INORGANIC
 CC CATIONS.
 CC -!- SUBUNIT: FORMS OLIGOMERS IN ITS NATIVE STATE.
 CC -!- SIMILARITY: BELONGS TO THE GAMMA-PUROTHIONIN FAMILY.
 DR PIR; S28992; S28992.
 DR HSP; P30231; IAYU.
 DR InterPro; IPR002118; Gamma-thionin.
 DR ProDom; PD002594; Gamma-thionin; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; PARTIAL.
 KW Fungicide.
 FT MOD_RES 1 1
 FT NON_TER 23 23
 FT SEQUENCE 23 AA; 2467 MW; A11D4A9E364F5735 CRC64;

Query Match 20.1%; Score 27; DB 1; Length 23;
 Best Local Similarity 28.6%; Pred. No. 5.3e+02;
 Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 GTFQNTTSSTDCR 18

Db 9 GTWSGVCNNACK 22
 I : I : I :

RESULT 3
 CP23_SPOER STANDARD; PRT; 23 AA.
 AC P56683;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CARDIOACTIVE PEPTIDE CAP23.
 OS Spodoptera eridania (Southern armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=37547;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=99196260; PubMed=10098624;
 RA Furuya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H.,
 RA Shabanowitz J., Hunt D.F., Schooley D.A.;
 RT "A cardioactive peptide from the southern armyworm, Spodoptera
 eridania.";
 RL Peptides 20:53-61(1999).
 CC -!- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM
 CC LARVAL MANDUCA SEXTA. CAUSING AN INOTROPIC EFFECT AT LOW
 CC CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
 CC AT HIGH DOSES.
 CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 DR InterPro; IPR003463; GBP_PSP.
 DR Pfam; PF02425; GBP_PSP; 1.
 FT DISULFID 7
 FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;
 BY SIMILARITY.

Query Match 19.0%; Score 25.5; DB 1; Length 23;
 Best Local Similarity 33.3%; Pred. No. 8.8e+02;
 Matches 6; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

QY 2 CAPQTFNTTSSTDCRP 19
 I : I : I :
 DB 7 CTPG-YQTADGR--CRP 21

RESULT 4
 PAP2_SPOEX STANDARD; PRT; 23 AA.
 AC P30256;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE II (pp II).
 OS Spodoptera exigua (Beet armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7107;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 Heliothis virescens.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 DR PIR; D39855; D39855.

DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA; 2477 MW; 0A96CB4600855AE0 CRC64;

Query Match 19.0%; Score 25.5; DB 1; Length 23;
 Best Local Similarity 33.3%; Pred. No. 8.8e+02;
 Matches 6; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

OY 2 CAPGTFSTSTSDICRP 19
 | | | : | : |
 Db 7 CTPG-YQTADGR--CKP 21

RESULT 5

ID P3_SPOEX STANDARD; PRT; 23 AA.
 AC P30257;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE III (PP III).
 OS Spodoptera exigua (Beet armyworm).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Noctuoidea; Noctuidae; Amphipyridae; Spodoptera.
 OX NCBI_TaxID=7107;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens."
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING. FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE GBP / PSPI / PARALYTIC PEPTIDE FAMILY.
 DR PIR: E39855; E39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; 1.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA; 2505 MW; 0A96CB5EB7D55AE0 CRC64;

Query Match 19.0%; Score 25.5; DB 1; Length 23;
 Best Local Similarity 33.3%; Pred. No. 8.8e+02;
 Matches 6; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

OY 2 CAPGTFSTSTSDICRP 19
 | | | : | : |
 Db 7 CTPG-YQTADGR--CKP 21

RESULT 6

ID TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: S23307; S23307.
 DR PIR: S23308; S23308.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 18.7%; Score 25; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 RPHQ 21
 | | | |
 Db 3 RPHQ 6

RESULT 7

ID CXM2_CONGE STANDARD; PRT; 22 AA.
 AC P01524;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE MU-CONOTOXIN GLIIB (MYOTOXIN II) (GEOGRAPHUTOXIN II) (GTX-II).
 OS Conus geographus (Geography cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85261316; PubMed=2410412;
 RA Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
 RA Yoshikami D., Moczydlowski E.;
 RT "Conus geographus toxins that discriminate between neuronal and
 RT muscle sodium channels."
 RL J. Biol. Chem. 260:9280-9288(1985).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=83210170; PubMed=6852238;
 RA Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.;
 RT "The amino acid sequences of homologous hydroxyproline-containing
 RT myotoxins from the marine snail Conus geographus venom."
 RL FEBS Lett. 155:277-280(1983).
 RN [3]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails."
 RL Annu. Rev. Biochem. 57:665-700(1988).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96280640; PubMed=8688418;
 RA Hill J.M., Alewood P.F., Craik D.J.;
 RT "Three-dimensional solution structure of mu-conotoxin GIIB, a
 RT specific blocker of skeletal muscle sodium channels.";

RL Biochemistry 35:8824-8835(1996).
 CC -I- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK
 CC MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
 CC CHANNELS.
 DR PIR: A01787; MXKN2
 DR PIR: B23579; B23579.
 DR PDB: 1GIB; 08-NOV-96.
 KW Sodium channel inhibitor; Hydroxylation; Amidation; Venom;
 KW 3D-structure.
 FT DISULFID 3 15
 FT DISULFID 4 20
 FT DISULFID 10 21
 FT MOD_RES 6 6
 FT MOD_RES 7 7
 FT MOD_RES 17 17
 FT MOD_RES 22 22
 FT AMIDATION.
 SQ SEQUENCE 22 AA; 2599 MW; F50402BA93199E01 CRC64;

Query Match 18.7%; Score 25; DB 1; Length 22;
 Best Local Similarity 44.4%; Pred. No. 9.9e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 15 DICRPHQIC 23
 I I I I
 Db 2 DCCTPPK 10

RESULT 8
 CXM3_CONGE STANDARD; PRT; 22 AA.
 AC P05482;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE MU-CONOTOXIN GIIC.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85261316; PubMed=2410412;
 RA Cruz L.J., Gray W.R., Olivera B.M., Zelkus R.D., Kerr L.,
 RA Yoshikami D., Moczydlowski E.;
 RT "Conus geographus toxins that discriminate between neuronal and
 RT muscle sodium channels.";
 RL J. Biol. Chem. 260:9280-9288(1985).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -I- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK
 CC MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
 CC CHANNELS.

DR PIR: C23579; C23579.
 DR HSP; P01524; 1GIB.
 KW Sodium channel inhibitor; Hydroxylation; Amidation; Venom.
 FT DISULFID 3 15
 FT DISULFID 4 20
 FT DISULFID 10 21
 FT MOD_RES 6 6
 FT MOD_RES 7 7
 FT MOD_RES 17 17
 FT MOD_RES 22 22
 FT AMIDATION.
 SQ SEQUENCE 22 AA; 2553 MW; F50402BA92A9813C CRC64;

Query Match 18.7%; Score 25; DB 1; Length 22;
 Best Local Similarity 44.4%; Pred. No. 9.9e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 15 DICRPHQIC 23
 I I I I
 Db 2 DCCTPPK 10

RESULT 9
 LANM_STRMU STANDARD; PRT; 22 AA.
 AC P80666;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE LANTIBIOTIC MUTACIN B-NY266.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=NY266;
 RX MEDLINE=97379322; PubMed=9237644;
 RA Mota-Meira M., Lacroix C., Lapointe G., Lavole M.C.;
 RT "Purification and structure of mutacin B-NY266: a new lantibiotic
 RT produced by Streptococcus mutans.";
 RL FEBS Lett. 410:275-279(1997).
 CC -I- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC)
 CC ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF
 CC LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL
 CC CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
 CC TRANSMEMBRANE PORES.
 CC -I- MASS SPECTROMETRY: MW=2270.29; MW_ERR=0.21; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
 DR InterPro: IPR001049; Gallidermin.
 DR Pfam: PF02052; Gallidermin; 1.
 DR PRINTS; PR00323; GALLIDERMIN.
 KW Antibiotic; Bacteriocin; Lantibiotic; Plasmid.
 FT MOD_RES 5 5
 FT MOD_RES 8 8
 FT MOD_RES 14 14
 FT MOD_RES 19 19
 FT THIOETH 3 7
 FT THIOETH 8 11
 FT THIOETH 16 21
 FT THIOETH 19 22
 FT THIOETH 22 AA; 2425 MW; 96IC1480401F92CE CRC64;
 SQ SEQUENCE

Query Match 18.3%; Score 24.5; DB 1; Length 22;
 Best Local Similarity 37.5%; Pred. No. 1.2e+03;
 Matches 6; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 CAPGTFSTNTSSSTDIC 17
 I I I I I I I
 Db 7 CTGCG-AKTGSFNSYC 21

RESULT 10
 HBB2_UROHA STANDARD; PRT; 19 AA.
 AC P18992;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE HEMOGLOBIN BETA-2 CHAIN (FRAGMENT).
 OS Uromastix hardwickii (Indian spiny-tailed lizard).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
 OC Uromastix.
 OX NCBI_TaxID=40250;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84029159; PubMed=6628672;

RA Naqvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
 RA Joernvall H.;
 RT "Characterization of hemoglobin from the lizard Uromastix
 RT hardwickii.";
 RL FEBS Lett. 162:290-295(1983).
 DR PIR: A05305; A05305.
 DR InterPro: IPR000971; Globin.
 DR PROSITE: PS01033; GLOBIN; PARTIAL.
 KW Heme; Oxygen transport; Respiratory protein; Erythrocyte.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1914 MW; C40AD8EA30019057 CRC64;

Query Match 17.9%; Score 24; DB 1; Length 19;
 Best Local Similarity 41.7%; Pred. No. 1.2e+03;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTFSNTSTSDI 16
 DB 3 GDFGNISAAAI 14
 |||:|:|
 |||:|:|

RESULT 11
 DCMW_PSECA STANDARD; PRT; 15 AA.
 AC P19920;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] MEDIUM CHAIN (EC 1.2.2.4)
 DE (FRAGMENT).
 OS Pseudomonas carboxydovorans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group; Oligotropa.
 OX NCBI_TaxID=40137;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=OM5;
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydotropic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC 2 H(+) + FERRICYTOCHROME B-561.
 CC -|- CATALYTIC ACTIVITY: CO + H(2)O + FERROCYTOCHROME B-561 +
 CC -|- COPRODUCT: MOLYBDENUM.
 CC -|- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: P10141; P10141.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1779 MW; 82DD3BF93E739D63 CRC64;

Query Match 17.5%; Score 23.5; DB 1; Length 15;
 Best Local Similarity 36.8%; Pred. No. 1.1e+03;
 Matches 7; Conservative 1; Mismatches 4; Indels 7; Gaps 1;

QY 4 PGTFSTSTSDICRPHQI 22
 |||:|:|
 DB 4 PGSF-----DYHRPKSI 15

RESULT 12
 CXAB_CONPE STANDARD; PRT; 16 AA.
 AC P50985;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ALPHA-CONOTOXIN PNIB.
 OS Conus pennaceus.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Venom;
 MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Fainzilber M., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors.";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP SULFATION OF TYR-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=97444322; PubMed=9298951;
 RA Hu S.H., Gehrman J., Alewood P.F., Craik D.J., Martin J.L.;
 RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
 RT comparison with alpha-conotoxins PnIA and GI.";
 RL Biochemistry 36:11323-11330(1997).
 CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
 DR PDB; LAG; 20-MAY-98.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Sulfation; Venom; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;
 Query Match 17.5%; Score 23.5; DB 1; Length 16;
 Best Local Similarity 35.3%; Pred. No. 1.2e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 7; Gaps 1;
 QY 1 PCAPGTFSTSTSDIC 17
 |||:|:|
 DB 7 PCA-----LSNPDYC 16

RESULT 13
 HELT_HELHO STANDARD; PRT; 20 AA.
 AC P46693;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HELOTHERMINE (FRAGMENT).
 OS Heloderma horridum horridum (Mexican beaded lizard).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
 OC Heloderma.
 OX NCBI_TaxID=8552;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Venom;
 MEDLINE=90260878; PubMed=1693019;
 RA Mochca-Morales J., Martin B.M., Possani L.D.;
 RT "Isolation and characterization of helothermine, a novel toxin from

RT Heloderma horridum horridum (Mexican beaded lizard) venom."
 RL Toxinon 28:299-309(1990).
 CC -1- FUNCTION: TOXIC TO MICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF
 CC REAR LIMBS AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT
 CC MIGHT BE A HYPOTHERMIC TOXIN.
 CC -1- MISCELLANEOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 KDA
 CC AND A PI OF 6.8.
 DR PIR; A34859; A34859.
 KW Toxin.
 FT NON-TER
 SQ SEQUENCE 20 AA; 2156 MW; 91D62B36F7B4F940 CRC64;

Query Match 17.5%; Score 23.5; DB 1; Length 20;
 Best Local Similarity 41.2%; Pred. No. 1.5e+03;
 Matches 7; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 1 PCAPGTF-SNVTSTDI 16
 I I I I I I
 Db 4 PKLPLGLMTSNPDQQTET 20

RESULT 14

PAP1_HELVI STANDARD; PRT; 23 AA.
 AC P30251;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PARALYTIC PEPTIDE I (PP I).
 OS Heliothis virescens (Noctuid moth) (Owlet moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
 OX NCBI_TaxID=7102;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S.; Dennis P.A.; Li J.P.; Summerfelt R.M.; Carney R.L.;
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens."
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 DR PIR; F39855; F39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; I.
 KW Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA; 2524 MW; 2236CB436D655AFA CRC64;

Query Match 17.5%; Score 23.5; DB 1; Length 23;
 Best Local Similarity 33.3%; Pred. No. 1.7e+03;
 Matches 6; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

QY 2 CAPGTFSTSTSDICRP 19
 I I I I I I
 Db 7 CIPG-YMRTADGR--CKP 21

RESULT 15

PAP2_HELVI STANDARD; PRT; 23 AA.
 AC P30252;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE PARALYTIC PEPTIDE II (PP II).
 OS Heliothis virescens (Noctuid moth) (Owlet moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
 OX NCBI_TaxID=7102;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=91302298; PubMed=2071576;
 RA Skinner W.S.; Dennis P.A.; Li J.P.; Summerfelt R.M.; Carney R.L.;
 RA Quistad G.B.;
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
 RT Heliothis virescens."
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC PIR; G39855; G39855.
 DR InterPro: IPR003463; GBP_PSP.
 DR Pfam: PF02425; GBP_PSP; I.
 KW Hemolymph.
 SQ SEQUENCE 23 AA; 2508 MW; 2236CB5D6C855AFA CRC64;

Query Match 17.5%; Score 23.5; DB 1; Length 23;
 Best Local Similarity 33.3%; Pred. No. 1.7e+03;
 Matches 6; Conservative 2; Mismatches 7; Indels 3; Gaps 2;

QY 2 CAPGTFSTSTSDICRP 19
 I I I I I I
 Db 7 CIPG-YMRTADGR--CKP 21

Search completed: February 12, 2002, 13:06:44
 Job time: 168 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 13:04:16 ; Search time 22.01 seconds
(without alignments)
152.852 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_185

Perfect score: 134

Sequence: 1 PCAPGTFSTSTSDICRPHQIC 23

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 6766

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL.17.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_phase.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	24.6	15	11 Q9QUV5	Q9quv5 rattus sp.
2	30	22.4	20	12 Q78505	Q78505 human immun
3	29	21.6	17	12 Q78381	Q78381 human immun
4	29	21.6	18	12 Q9QEX3	Q9qex3 human immun
5	29	21.6	21	4 Q16017	Q16017 homo sapien
6	28	20.9	17	12 Q78323	Q78323 human immun
7	28	20.9	17	12 Q78378	Q78378 human immun
8	28	20.9	17	12 Q78327	Q78327 human immun
9	28	20.9	17	12 Q78380	Q78380 human immun
10	28	20.9	21	5 Q25086	Q25086 herdmamia m
11	28	20.9	23	5 Q25134	Q25134 haliotis ru
12	27	20.1	17	12 Q78379	Q78379 human immun
13	27	20.1	20	2 Q96173	Q96173 vibrio sp.
14	27	20.1	20	5 Q9TWR5	Q9twr5 phoneutria
15	27	20.1	22	13 Q91102	Q91102 morone saxa
16	27	20.1	23	12 Q86611	Q86611 human immun
17	26	19.4	15	5 Q26159	Q26159 plasmodium
18	26	19.4	20	6 Q9TRH7	Q9trh7 canis famli
19	26	19.4	20	10 Q9S885	Q9s885 lupinus alb

20	26	19.4	20	11	Q9QVD6	Q9qv6 rattus sp.
21	26	19.4	21	3	Q9UTM6	Q9utt6 schizosacch
22	26	19.4	22	3	Q9UB51	Q9ur51 filobesidie
23	26	19.4	23	5	P90716	P90716 berce ovata
24	26	19.4	23	12	Q9QEX5	Q9qex5 human immun
25	26	19.4	23	12	Q9QEX4	Q9qex4 human immun
26	25.5	19.0	22	4	Q13726	Q13726 homo sapien
27	25	18.7	13	10	Q9S922	Q9s922 brassica ol
28	25	18.7	13	11	P97944	P97944 mus musculus
29	25	18.7	17	5	Q9TWC6	Q9twc6 dirofilaria
30	25	18.7	18	4	Q9UCN8	Q9ugn8 homo sapien
31	25	18.7	19	10	Q9S923	Q9s923 brassica ol
32	25	18.7	20	12	Q78486	Q78486 human immun
33	25	18.7	20	12	Q78507	Q78507 human immun
34	25	18.7	20	12	Q78508	Q78508 human immun
35	25	18.7	20	12	Q78509	Q78509 human immun
36	25	18.7	22	3	Q9Y8F8	Q9y8f8 glomus moss
37	24.5	18.3	15	4	Q93046	Q93046 homo sapien
38	24	17.9	15	2	O69142	O69142 streptococc
39	24	17.9	15	10	Q9S8B9	Q9s8b9 lupinus alb
40	24	17.9	16	4	Q9UC48	Q9uc48 homo sapien
41	24	17.9	16	4	Q9NPO7	Q9npq7 homo sapien
42	24	17.9	16	13	Q9PRU6	Q9pru6 gallus gall
43	24	17.9	17	12	O85719	O85719 reovirus sp
44	24	17.9	17	12	Q78345	Q78345 human immun
45	24	17.9	17	13	Q9PRU7	Q9pru7 gallus gall

ALIGNMENTS

RESULT 1

Q9QUV5 ID Q9QUV5 PRELIMINARY: PRT; 15 AA.

AC Q9QUV5; Q9QUV5; 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE OLIGODENDROCYTE-SPECIFIC UDP-GALACTOSE: CERAMIDE GALACTOSYLTRANSFERASE

DE (FRAGMENT).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE.

RX MEDLINE=96085162; PubMed=8521863;

RA Schulte S., Stoffel W.;

RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate

RT transporter. Copurification, separation and characterization of the

RT two glycoproteins."

RL Eur. J. Biochem. 233:947-953(1995).

SQ SEQUENCE 15 AA; 1657 MW; 84474749A06BF6CC CRC64;

Query Match 24.6%; Score 33; DB 11; Length 15;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PGTFSTNTS 12

||| :|||

Db 2 PGIFXSTTS 10

RESULT 2

Q78505 ID Q78505 PRELIMINARY: PRT; 20 AA.

AC Q78505;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE VIRAL SAMPLE FLO5R5D (FLORIDA LOCAL CONTROL 01), PARTIAL ENV CDS, V5

DE REGION (FRAGMENT).

RESULT 4
Q9QEX3

RESULT	6
Q78323	
ID	Q78323
	PRELIMINARY;
AC	Q78323;
DT	01-NOV-1996 (TRENBLrel. 01, Created)
	PRT;
	17 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VIRAL SAMPLE FLPAR5A (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION
DE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
RA Curran J.W., Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice."
RL Science 256:1165-1171(1992).
DR EMBL; M92109; AAA44465.1; -;
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1649 MW; 3B857BBFD12CA370 CRC64;

Query Match 20.9%; Score 28; DB 12; Length 17;
Best Local Similarity 45.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSSTDICRP 19
| | : | : |
Db 3 NNTNGTETFRP 13

RESULT 7
Q78378
ID Q78378 PRELIMINARY; PRT; 17 AA.
AC Q78378;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VIRAL SAMPLE FLPAR5A (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
DE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
RA Curran J.W., Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice."
RL Science 256:1165-1171(1992).
DR EMBL; M92123; AAA44493.1; -;
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1723 MW; 34757935D12CA370 CRC64;

Query Match 20.9%; Score 28; DB 12; Length 17;
Best Local Similarity 45.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSSTDICRP 19
| | : | : |
Db 3 NNTNGTETFRP 13

RESULT 8
Q78327
ID Q78327 PRELIMINARY; PRT; 17 AA.
AC Q78327;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VIRAL SAMPLE FLPAR5D (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION
DE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
RA Curran J.W., Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice."
RL Science 256:1165-1171(1992).
DR EMBL; M92112; AAA44468.1; -;
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1651 MW; 34757BBFD12CA370 CRC64;

Query Match 20.9%; Score 28; DB 12; Length 17;
Best Local Similarity 45.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSSTDICRP 19
| | : | : |
Db 3 NNTNGTETFRP 13

RESULT 9
Q78380
ID Q78380 PRELIMINARY; PRT; 17 AA.
AC Q78380;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VIRAL SAMPLE FLPAR5E (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
DE (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
RA Curran J.W., Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice."
RL Science 256:1165-1171(1992).
DR EMBL; M92125; AAA44495.1; -;
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1651 MW; 34757BBFD12CA370 CRC64;

::

Query Match 20.9%; Score 28; DB 12; Length 17;
Best Local Similarity 45.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSTSDICRP 19
| : | : |
Db 3 NNTNGTETFRP 13

RESULT 10

Q25086 ID Q25086 PRELIMINARY; PRT; 21 AA.
AC Q25086;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CLONE AHOX4 HOMEBOX PROTEIN (FRAGMENT).
OS Herdmania momus.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Herdmania.
OX NCBI_TaxID=7733;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Kennett C.V.D.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09939; AAA18629.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
FT NON_TER 21
SQ SEQUENCE 21 AA; 2650 MW; AB7FF3AF1FA659C3 CRC64;

Query Match 20.9%; Score 28; DB 5; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 16 ICRPHQI 22
| : | : |
Db 4 LCRPRRI 10

RESULT 11

Q25134 ID Q25134 PRELIMINARY; PRT; 23 AA.
AC Q25134;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE HROX3 (FRAGMENT).
GN HROX3.
OS Haliotis rufescens (California red abalone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Haliotidae; Haliotis.
OX NCBI_TaxID=6454;
RN [1]
RP SEQUENCE FROM N.A.
RA Degnan B.M.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93372986; PubMed=7689904;
RA Degnan B.M.; Morse D.E.;
RT "Identification of eight homeobox-containing transcripts expressed during larval development and at metamorphosis in the gastropod mollusc Haliotis rufescens."
RT Mol. War. Biol. Biotechnol. 2:1-9(1993).
DR EMBL; X79372; CAA55917.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00046; homeobox; 1.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2793 MW; CC387AE7BDA6C44D CRC64;

Query Match 20.9%; Score 28; DB 5; Length 23;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 16 ICRPHQI 22
| : | : | : |
Db 5 LCRPRRI 11

RESULT 12

Q78379 ID Q78379 PRELIMINARY; PRT; 17 AA.
AC Q78379;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE VIRAL SAMPLE FLPR5C (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C., Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L., Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A., Curran J.W., Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice."
RL Science 256:1165-1171(1992).
DR EMBL; M92124; AAA44494.1; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1652 MW; 34757BBFD1240170 CRC64;

Query Match 20.1%; Score 27; DB 12; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSTSDICRP 19
| : | : | : |
Db 3 NDTNGTETFRP 13

RESULT 13

P96173 ID P96173 PRELIMINARY; PRT; 20 AA.
AC P96173;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE LEADER PEPTIDE.
OS Vibrio sp. (strain 2693).
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=79682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2693;
RX MEDLINE=98274751; PubMed=9611817;
RA Xu Y., Zhang Y., Liang Z.Y., Van de Castele M., Legrain C., Glansdorff N.;
RT "Aspartate carbamoyltransferase from a psychrophilic deep-sea

RT bacterium, Vibrio strain 2693: properties of the enzyme, genetic
 RT organization and synthesis in *Escherichia coli*.;
 RL Microbiology 144:1435-1441(1998).
 DR EMBL: Y09786; CAA70922.1; -.
 SQ SEQUENCE 20 AA; 2241 MW; 35C31F588FB85D63 CRC64;

Query Match 20.1%; Score 27; DB 2; Length 20;
 Best Local Similarity 41.7%; Pred. No. 1.6e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSSTDICRP 20
 :: || : |||
 Db 7 SLSLSPKLVLRPH 18

RESULT 14

Q9TWR5 PRELIMINARY; PRT; 20 AA.
 AC Q9TWR5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PNV2 TOXIN (FRAGMENT).
 OS Phoneutria nigriventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
 OX NCBI_TaxID=6918;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94030062; PubMed=8216354;
 RA Bento A.C., Novello J.C., Marangoni S., Antunes E., Giglio J.R.,
 RA Oliveira B., de Nucci G.;
 RT "Identification of a new vascular smooth muscle contracting
 RT polypeptide in *Phoneutria nigriventer* spider venom.";
 RL Biochem. Pharmacol. 46:1092-1095(1993).
 SQ SEQUENCE 20 AA; 2176 MW; F28C3D81D983BCA5 CRC64;

Query Match 20.1%; Score 27; DB 5; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 DICRP 19
 |||:
 Db 6 DICQP 10

RESULT 15

Q91102 PRELIMINARY; PRT; 22 AA.
 AC Q91102;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HOX-B3-LIKE HOMEODOMAIN PROTEIN (FRAGMENT).
 OS Morone saxatilis (Striped bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
 OC Moronidae; Morone.
 OX NCBI_TaxID=34816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=95005122; PubMed=7921046;
 RA Pavell A.M., Stellwag E.J.;
 RT "Survey of Hox-like genes in the teleost *Morone saxatilis*:
 RT implications for evolution of the Hox gene family.";
 RL Mol. Mar. Biol. Biotechnol. 3:149-157(1994).
 DR EMBL: U09944; AAC59650.1; -.
 DR HSSP: P02833; 9ANT.
 DR InterPro: IPR001356; Homeobox.

DR Pfam: PF00046; homeobox; 1.
 KW Homeobox; Nuclear protein; DNA-binding.
 FT NON_TER 1
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2703 MW; AE4485CB7FF7CF1D CRC64;

Query Match 20.1%; Score 27; DB 13; Length 22;
 Best Local Similarity 42.9%; Pred. No. 1.7e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 ICRPHQI 22
 :||| :
 Db 2 LCRPRRV 8

Search completed: February 12, 2002, 13:07:13
 Job time: 177 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 13:00:40 ; Search time 23.63 Seconds
(without alignments)
72.098 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_185

Perfect score: 134

Sequence: 1 PCAPGTFSTSTSDICRPHQIC 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 213999

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	34.3	17	20	AAW95323
2	41	30.6	17	21	AAV51961
3	41	30.6	17	21	AAV51973
4	37	27.6	22	21	AAV51542
5	37	27.6	23	20	AAW73416
6	34.5	25.7	17	22	AAU05310
7	34.5	25.7	18	22	AAU05309
8	34.5	25.7	20	22	AAU05307
9	34.5	25.7	20	22	AAU05315
10	34.5	25.7	21	22	AAU05308
11	34.5	25.7	23	19	AAW65481

12	34	25.4	20	22	AAU05353	R1 and R2 peptide
13	33.5	25.0	20	21	AAV23019	Human APC protein
14	33	24.6	15	19	AAV20893	Human presenilin I
15	33	24.6	16	16	AAV75932	Dextranase N-termi
16	33	24.6	20	22	AAU05317	R1 and R2 peptide
17	33	24.6	20	22	AAU05346	R1 and R2 peptide
18	33	24.6	20	22	AAU05356	R1 and R2 peptide
19	33	24.6	20	22	AAU05359	R1 and R2 peptide
20	33	24.6	20	22	AAU05390	R1 and R2 peptide
21	32.5	24.3	23	6	AAV50661	Sequence of Immuno
22	32.5	24.3	23	20	AAV28912	MSF 1-alpha peptid
23	32	23.9	15	18	AAW07656	Human ATM gene pro
24	32	23.9	15	18	AAW06235	ATM epitope #1. H
25	32	23.9	15	19	AAW77164	Pharmaceutically a
26	32	23.9	15	20	AAV33126	Human umbilical co
27	32	23.9	15	22	AAV62281	ATM open reading f
28	32	23.9	16	20	AAV14391	Peptide #19 for ep
29	32	23.9	16	20	AAV15781	Antigenic peptide
30	32	23.9	17	21	AAV59437	Human delta3 fragm
31	32	23.9	20	21	AAV65710	TGF beta 2 mutant
32	32	23.9	22	18	AAV26538	Erythropoietin rec
33	31.5	23.5	18	22	AAU05323	R1 and R2 peptide
34	31.5	23.5	20	22	AAU05325	R1 and R2 peptide
35	31	23.1	10	22	AAV95723	Human complementar
36	31	23.1	15	20	AAV08939	Fibronectin-like s
37	31	23.1	15	21	AAV52487	Fibronectin-derive
38	31	23.1	18	22	AAV98822	Human cell death p
39	31	23.1	20	12	AAV15600	Immunopeptide deri
40	31	23.1	20	16	AAV84512	Hepatitis C virus
41	31	23.1	20	17	AAV91006	HCV E2 peptide E2-
42	31	23.1	20	22	AAU05360	R1 and R2 peptide
43	31	23.1	20	22	AAU05381	R1 and R2 peptide
44	30.5	22.8	20	22	AAV15022	Peptide #1456 enco
45	30.5	22.8	20	22	AAV27460	Peptide #1497 enco

ALIGNMENTS

RESULT 1

AAW95323
ID AAW95323 standard; Protein; 17 AA.

AC AAW95323;

DT 15-MAR-1999 (first entry)

DE Costant and variable domain sequence of C. psittaci CPS92-106.

XX Chlamydia; cryptic phase; elementary body phase; replicating; probenicid;
KW antiporphyrin acid; immune response; infection; diagnostic; assay; MOMP;
KW major outer membrane protein; autoimmune; inflammatory; porphyria;
KW Ebstein Barr virus; antioxidant.

OS Chlamydia psittaci.

XX WO9850074-A2.

XX 12-NOV-1998.

XX 06-MAY-1998; 98WO-US09237.

XX 18-FEB-1998; 98US-0025521.

XX 06-MAY-1997; 97US-0045689.

XX 06-MAY-1997; 97US-0045739.

XX 06-MAY-1997; 97US-0045779.

XX 06-MAY-1997; 97US-0045780.

XX 06-MAY-1997; 97US-0045784.

XX 06-MAY-1997; 97US-0045787.

XX 14-AUG-1997; 97US-0911593.

XX 18-FEB-1998; 98US-0025174.

XX 18-FEB-1998; 98US-0025176.

PA (UYVA-) UNIV VANDERBILT.
 XX Mitchell WM, Stratton CW;
 XX WPI; 1999-059653/05.
 XX Composition with two agents effective against different stages of
 PT chlamydial life cycle - comprises agent targetted against cryptic
 PT phase, against elementary body phase, against replicating phase,
 PT probenicid and antiporphyrin
 XX
 XX Claim 4; Fig 3; 138pp; English.
 XX
 CC The invention relates to the diagnosis and management of infections by
 CC Chlamydia species. The invention provides a composition that comprises
 CC at least two agents, where each of the agents is effective against a
 CC different phase of the chlamydial life cycle. The agents are selected
 CC from: (a) agents targetted against cryptic phase of chlamydial life
 CC cycle; (b) agents targetted against elementary body phase of chlamydial
 CC life cycle; (c) agents targetted against replicating phase of chlamydial
 CC life cycle; (d) probenicid, and (e) antiporphyrin acid. The composition
 CC is used to elicit a protective immune response to Chlamydia infection in
 CC an animal or human and is applied until the animal or human tests
 CC negative for Chlamydia infection. It is also used to treat biological
 CC material infected with Chlamydia. Diagnostic kits for antibody assays
 CC against recombinant major outer membrane protein (MOMP), and for DNA
 CC amplification assays for chlamydial genes, are used to diagnose disease,
 CC e.g. autoimmune disease, an inflammatory disease or a disease that
 CC occurs in an immuno-compromised individual, associated with Chlamydia
 CC infection. The kits are used to detect chlamydial elementary bodies in a
 CC sample. They are also used to monitor and/or modify the course of therapy
 CC in a patient. The treatment reduces the acellular load of infectious
 CC Epstein Barr virus. The method is also used to treat porphyria, by
 CC reducing the number of elementary bodies and applying a drug, e.g.
 CC cimetidine, and antioxidants, to reduce the adverse effects associated
 CC with porphyria. Sequences AAW95320 to AAW95323 represent constant and
 CC variable domain sequences of various Chlamydia species.
 XX
 XX Sequence 17 AA;

Query Match 34.3%; Score 46; DB 20; Length 17;
 Best Local Similarity 64.3%; Pred. No. 5;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 CAPGTFSTSTSD 15
 II II IIII :
 Db 1 casgtsantvaad 14

RESULT 2
 AAY51961
 ID AAY51961 standard; peptide; 17 AA.
 XX
 XX AAY51961;
 XX
 XX 23-JUN-2000 (first entry)
 XX
 XX P. pastoris lysyl oxidase peptide fragment #11.
 DE
 XX Lysyl oxidase; lipoxxygenase; protein disulfide isomerase; phenol oxidase;
 KW peroxidase; protein disulfide reductase; tyrosine oxidase; fodder;
 KW sulfhydryl oxidase; food additives.
 XX
 XX Pichia pastoris.
 OS
 XX DE19840069-A1.
 PN
 XX 09-MAR-2000.
 PD
 XX 03-SEP-1998; 98DE-1040069.
 PF
 XX 03-SEP-1998; 98DE-1040069.
 PR

XX (BADI) BASF AG.
 XX
 XX Friedrich T, Bewert W, Lueddecke E, Klingler J, Heger R;
 XX WPI; 2000-257743/23.
 XX
 XX Manufacture of active preparations comprises cross linking a protein,
 PT which surrounds the active substance with an enzyme, especially a novel
 PT lysyl oxidase from Pichia pastoris
 XX
 XX Claim 17; Page 17; 22pp; German.
 PS
 XX
 CC This invention describes a novel method to manufacture a preparation of
 CC an active substance, where the active substance is surrounded by at
 CC least one layer consisting of a protein that is cross-linked by an
 CC enzyme chosen from the group of lipoxxygenase, protein disulfide
 CC isomerase, phenol oxidase and peroxidase, lysyl oxidase, protein
 CC disulfide reductase, tyrosine oxidase or sulfhydryl oxidases. Enzymes
 CC chosen from lipoxxygenase, protein disulfide isomerase, phenol oxidase
 CC and peroxidase, protein disulfide reductase, tyrosine oxidase or
 CC sulfhydryl oxidases, especially lysyl oxidase are useful for formulation
 CC of preparations of active substances. The method of the invention is
 CC used for manufacturing preparations of active substances. The
 CC preparations are useful as food additives or fodder or as
 CC pharmaceuticals. AAY51951-Y51962 represent fragments of the Pichia
 CC pastoris lysyl oxidase which are used to illustrate the method of the
 CC invention.

XX Sequence 17 AA;
 SQ
 Query Match 30.6%; Score 41; DB 21; Length 17;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 PCAPGTFSTNT 10
 IIIII II
 Db 7 pcapgvvynt 16

RESULT 3
 AAY51973
 ID AAY51973 standard; peptide; 17 AA.
 XX
 XX AAY51973;
 XX
 XX 23-JUN-2000 (first entry)
 XX
 XX P. pastoris lysyl oxidase fragment #11.
 DE
 XX Lysyl oxidase; lipoxxygenase; protein disulfide isomerase; phenol oxidase;
 KW peroxidase; protein disulfide reductase; tyrosine oxidase; food;
 KW sulfhydryl oxidase; animal feed.
 XX
 XX Pichia pastoris.
 OS
 XX DE19840489-A1.
 PN
 XX 09-MAR-2000.
 PD
 XX 04-SEP-1998; 98DE-1040489.
 PF
 XX 04-SEP-1998; 98DE-1040489.
 PR
 XX (BADI) BASF AG.
 XX
 XX Friedrich T, Bewert W, Lueddecke E, Klingler J, Heger R;
 XX WPI; 2000-272257/24.
 XX
 XX Use of specified enzymes, especially lysyl oxidase, as protein
 PT crosslinking agents for formulating compositions containing active

PT Ingredients -

PS Claim 17; Page 16; 20pp; German.

XX This invention describes a novel method where an enzyme (I) selected
 CC from lipxygenases, protein disulfide isomerases, phenol oxidases and
 CC peroxidases, lysyl oxidases, protein disulfide reductases, tyrosine
 CC oxidases or sulfhydryl oxidases is used to formulate compositions
 CC containing active ingredients. (I) is useful for crosslinking protein
 CC layers surrounding active ingredients in food, animal feed and
 CC pharmaceutical products. The compositions can be formulated without
 CC using chemical crosslinking agents. AAY51963-Y51974 represent fragments
 CC of the Pichia pastoris lysyl oxidase protein which is used to
 CC illustrate the method of the invention.

XX Sequence 17 AA;

Query Match 30.6%; Score 41; DB 21; Length 17;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PCAPGTFSTNT 10
 Db 7 pcapgvvynt 16
 ||||| ||

RESULT 4

AAB51542

ID AAB51542 standard; Peptide; 22 AA.

XX AAB51542;

XX 15-FEB-2001 (first entry)

XX Yada homologous peptide #5.

XX Proteobacteria; extracellular domain; virulence determinant; Yada;
 KW adhesin; proteobacterial infection prevention; vaccine.

XX Thiobacillus ferrooxidans.

XX WO200061165-A1.

XX 19-OCT-2000.

XX 13-APR-2000; 2000WO-US09866.

XX 13-APR-1999; 99US-0129073.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Lupas AN;

XX WPI; 2000-647397/62.

XX An isolated polypeptide conserved in proteobacterial extracellular
 PT domains used in the treatment and prevention of bacterial infections -

XX Example 5; Page 59; 85pp; English.

XX This invention relates to peptides AAB51512 - AAB51537 which represent
 CC conserved proteobacterial extracellular domains. Sequences
 CC AAB51538 - AAB51618 represent peptides homologous to Yada, a yersinia
 CC adhesin which is an important virulence determinant of the yersinia
 CC species. The invention includes an antibody which binds to the
 CC proteobacterial extracellular peptides, and an immunogenic composition
 CC containing the antibody used as a vaccine to prevent infection by a
 CC proteobacteria. The polypeptides and antibodies are useful in the
 CC treatment and prevention of proteobacterial infections. The polypeptides
 CC can also be used to identify compounds which antagonize the binding of a
 CC bacterial adhesion to its ligand. The host cell can be used to produce

CC the polypeptides in a suitable culture system. The composition can be
 CC used to vaccinate a patient against a proteobacterial infection.

XX Sequence 22 AA;

Query Match 27.6%; Score 37; DB 21; Length 22;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 10; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

Qy 3 APTGTFSTNTSTDICRPHQI 22

Db 5 aptglsgt--stdavngsql 22

||||| ||| |

RESULT 5

AAW73416

ID AAW73416 standard; Protein; 23 AA.

XX AAW73416;

XX 19-FEB-1999 (first entry)

XX Human secreted protein encoded by Gene No. 20.

XX Secreted protein; human; protein therapy; gene therapy; blood disorder;
 KW pathological condition; diagnosis; cancer; neurological disorder;
 KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
 KW immune system disorder; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; prostate disease; autoimmune disorder; AIDS.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX Misc-difference 23

XX /note= "unspecified amino acid"

XX PN WO9854206-A1.

XX PD 03-DEC-1998.

XX 28-MAY-1998; 98WO-US10868.

XX 29-AUG-1997; 97US-0056296.

XX 30-MAY-1997; 97US-0044039.

XX 30-MAY-1997; 97US-0048093.

XX 30-MAY-1997; 97US-0048101.

XX 30-MAY-1997; 97US-0048190.

XX 30-MAY-1997; 97US-0048356.

XX 30-MAY-1997; 97US-0050935.

XX 29-AUG-1997; 97US-0056250.

XX 29-AUG-1997; 97US-0056293.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Carter KC, Dillon PJ, Endress GA, Feng P, Ni J;

XX Rosen CA, Ruben SM, Yu G;

XX WPI; 1999-070209/06.

XX N-PSDB; AAV08830.

XX New isolated human genes - useful for diagnosis and treatment of,
 PT e.g. cancers, neurological disorders, immune diseases, developmental
 PT disorders or blood disorders

XX Claim 11; Page 157; 188pp; English.

XX This sequence is encoded by a cDNA of the invention, designated
 CC Gene No. 20. This sequence represents a human secreted protein, and is
 CC expressed ubiquitously, including T-cells and amygdala.
 CC The DNA sequences of the invention and their corresponding secreted
 CC polypeptides are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions

CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the DNA sequences.
 CC Specific uses are described for each of the DNA sequences and the encoded
 CC proteins, based on which tissues they are most highly expressed in, and
 CC include developing products for the diagnosis or treatment of cancer,
 CC tumours, neurological disorders, developmental abnormalities and foetal
 CC deficiencies, blood disorders, leukaemias, diseases of the immune system
 CC (including allergies or asthma), hepatic disease, Alzheimer's and
 CC cognitive disorders, schizophrenia, prostate diseases, autoimmune
 CC disorders and AIDS. The polypeptides are also useful for identifying
 CC their binding partners.
 XX
 SQ Sequence 23 AA;

Query Match 27.6%; Score 37; DB 20; Length 23;
 Best Local Similarity 43.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 CAPGTFSTNTSSSTDIC 17
 ||| |||
 Db 5 cgp9aagtaacsacac 20

RESULT 6
 AAU05310
 ID AAU05310 standard; peptide; 17 AA.

XX AC AAU05310;

XX DT 24-OCT-2001 (first entry)

XX DE R1 and R2 peptide #4 useful as erythropoietin receptor agonist.

XX KW Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
 KW renal failure; anaemia; chronic inflammatory disease;
 KW autoimmune disease; malignancy; red blood count.

XX OS Homo sapiens.

XX PN WO200138342-A2.

XX PD 31-MAY-2001.

XX PF 24-NOV-2000; 2000WO-US32224.

XX PR 24-NOV-1999; 99US-0449064.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Balu P;

XX WPI; 2001-417749/44.

XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by
 PT binding linking group with functional groups as initiation sites for
 PT peptide synthesis to support and synthesizing peptide segments -

PS Example 2-5; Fig 1; 43pp; English.

XX The present sequence for potential R1 and R2 peptide #4 can be used
 CC to form a peptide dimer that binds and activates the erythropoietin
 CC receptor (EPO-R). Various possible peptide sequences for R1 and R2
 CC (AAU05301-AAU05393) are described in the present invention. Also
 CC described is a method for synthesizing such peptide dimers which
 CC act as EPO-R agonists. The method is useful for synthesizing peptide
 CC dimers which are useful, in vitro, as tools for understanding the
 CC biological role of EPO, in the development of other compounds that bind
 CC to EPO-R, as commercial research reagents for various medical research
 CC and diagnostic applications, for detecting EPO receptors on living
 CC cells, for treatment of disorders associated with a deficiency of EPO,
 CC such as end-stage renal failure/dialysis, anaemia associated with AIDS
 CC and chronic inflammatory diseases, autoimmune diseases and malignancies,

CC and for boosting the red blood count of a patient prior to surgery.
 XX
 SQ Sequence 17 AA;

Query Match 25.7%; Score 34.5; DB 22; Length 17;
 Best Local Similarity 43.8%; Pred. No. 2.1e+02;
 Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 5 GTFS-NTTSSDTCRP 19
 ||| : |||
 Db 1 gtyshfpgltbvrp 16

RESULT 7

AAU05309
 ID AAU05309 standard; peptide; 18 AA.

XX AC AAU05309;

XX DT 24-OCT-2001 (first entry)

XX DE R1 and R2 peptide #3 useful as erythropoietin receptor agonist.

XX KW Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
 KW renal failure; anaemia; chronic inflammatory disease;
 KW autoimmune disease; malignancy; red blood count.

XX OS Homo sapiens.

XX PN WO200138342-A2.

XX PD 31-MAY-2001.

XX PF 24-NOV-2000; 2000WO-US32224.

XX PR 24-NOV-1999; 99US-0449064.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Balu P;

XX WPI; 2001-417749/44.

XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by
 PT binding linking group with functional groups as initiation sites for
 PT peptide synthesis to support and synthesizing peptide segments -

PS Example 2-5; Fig 1; 43pp; English.

XX The present sequence for potential R1 and R2 peptide #3 can be used
 CC to form a peptide dimer that binds and activates the erythropoietin
 CC receptor (EPO-R). Various possible peptide sequences for R1 and R2
 CC (AAU05301-AAU05393) are described in the present invention. Also
 CC described is a method for synthesizing such peptide dimers which
 CC act as EPO-R agonists. The method is useful for synthesizing peptide
 CC dimers which are useful, in vitro, as tools for understanding the
 CC biological role of EPO, in the development of other compounds that bind
 CC to EPO-R, as commercial research reagents for various medical research
 CC and diagnostic applications, for detecting EPO receptors on living
 CC cells, for treatment of disorders associated with a deficiency of EPO,
 CC such as end-stage renal failure/dialysis, anaemia associated with AIDS
 CC and chronic inflammatory diseases, autoimmune diseases and malignancies,
 CC and for boosting the red blood count of a patient prior to surgery.

XX Sequence 18 AA;

Query Match 25.7%; Score 34.5; DB 22; Length 18;
 Best Local Similarity 43.8%; Pred. No. 2.2e+02;
 Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 5 GTFS-NTTSSDTCRP 19

```

Db      2 gtyschfgpltbvcrp 17
      |.:| : |.:|||
RESULT 8
AAU05307
ID AAU05307 standard; peptide; 20 AA.
XX
AC AAU05307;
XX
DT 24-OCT-2001 (first entry)
XX
DE R1 and R2 peptide #1 useful as erythropoietin receptor agonist.
XX
KW Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
KW renal failure; anaemia; chronic inflammatory disease;
KW autoimmune disease; malignancy; red blood count.
XX
OS Homo sapiens.
XX
PN WO200138342-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US32224.
XX
PR 24-NOV-1999; 99US-0449064.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Balu P;
XX
XX WPI; 2001-417749/44.
XX
PT Synthesizing peptide dimer useful as erythropoietin receptor agonist by
PT binding linking group with functional groups as initiation sites for
PT peptide synthesis to support and synthesizing peptide segments -
XX
PS Example 1; Fig 1; 43pp; English.
XX
CC The present sequence for potential R1 and R2 peptide #1 can be used
CC to form a peptide dimer that binds and activates the erythropoietin
CC receptor (EPO-R). Various possible peptide sequences for R1 and R2
CC (AAU05301-AAU05393) are described in the present invention. Also
CC described is a method for synthesizing such peptide dimers which
CC act as EPO-R agonists. The method is useful for synthesizing peptide
CC dimers which are useful, in vitro, as tools for understanding the
CC biological role of EPO, in the development of other compounds that bind
CC to EPO-R, as commercial research reagents for various medical research
CC and diagnostic applications, for detecting EPO receptors on living
CC cells, for treatment of disorders associated with a deficiency of EPO,
CC such as end-stage renal failure/dialysis, anaemia associated with AIDS
CC and chronic inflammatory diseases, autoimmune diseases and malignancies,
CC and for boosting the red blood count of a patient prior to surgery.
XX
SQ Sequence 20 AA;

Query Match 25.7%; Score 34.5; DB 22; Length 20;
Best Local Similarity 43.8%; Pred. No. 2 5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 5 GTFS-NTTSSSTDICRP 19
Db |.:| : |.:|||
2 gtyschfgpltbvcrp 17

RESULT 10
AAU05308
ID AAU05308 standard; peptide; 21 AA.
XX
AC AAU05308;
XX
DT 24-OCT-2001 (first entry)
XX
DE R1 and R2 peptide #2 useful as erythropoietin receptor agonist.
XX
KW Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
KW renal failure; anaemia; chronic inflammatory disease;
KW autoimmune disease; malignancy; red blood count.
XX
OS Homo sapiens.
XX

```

PN WO200138342-A2.
 PD 31-MAY-2001.
 XX
 XX 24-NOV-2000; 2000WO-US32224.
 XX
 XX 24-NOV-1999; 99US-0449064.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Balu P;
 XX
 XX WPI; 2001-417749/44.
 DR
 XX
 XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by
 PT binding linking group with functional groups as initiation sites for
 PT peptide synthesis to support and synthesizing peptide segments -
 XX
 XX Example 10-12; Fig 1; 43pp; English.
 PS
 XX The present sequence for potential R1 and R2 peptide #2 can be used
 CC to form a peptide dimer that binds and activates the erythropoietin
 CC receptor (EPO-R). Various possible peptide sequences for R1 and R2
 CC (AAU05301-AAU05393) are described in the present invention. Also
 CC described is a method for synthesizing such peptide dimers which
 CC act as EPO-R agonists. The method is useful for synthesizing peptide
 CC dimers which are useful, in vitro, as tools for understanding the
 CC biological role of EPO, in the development of other compounds that bind
 CC to EPO-R, as commercial research reagents for various medical research
 CC and diagnostic applications, for detecting EPO receptors on living
 CC cells, for treatment of disorders associated with a deficiency of EPO,
 CC such as end-stage renal failure/dialysis, anaemia associated with AIDS
 CC and chronic inflammatory diseases, autoimmune diseases and malignancies,
 CC and for boosting the red blood count of a patient prior to surgery.
 XX
 XX Sequence 21 AA;

Query Match 25.7%; Score 34.5; DB 22; Length 21;
 Best Local Similarity 43.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
 QY 5 GTFS-NTSSTDICRP 19
 II:I :::II
 Db 2 gtyschfgltbvrp 17.

RESULT 11
 AAW65481
 ID AAW65481 standard; peptide; 23 AA.
 XX
 XX AAW65481;
 AC
 XX
 XX 12-OCT-1998 (first entry)
 DT
 XX
 XX Hepatitis B surface antigen derived peptide (IGP 1082).
 DE
 XX
 XX Annexin V; hepatitis B surface antigen; immunogen; vaccine;
 KW hepatitis delta virus; infection; HBsAg.
 XX
 XX Synthetic.
 OS
 OS Hepatitis b virus.
 XX
 XX WO9829442-A1.
 PN
 XX
 XX 09-JUL-1998.
 PD
 XX
 XX 23-DEC-1997; 97WO-EP07268.
 PF
 XX
 XX 11-JUL-1997; 97EP-0870103.
 PR
 XX 30-DEC-1996; 96EP-0870164.
 XX
 XX (INNO-) INNOGENETICS NV.

XX De Meyer S, Depla E, Maertens G, Yap S;
 PI WPI; 1998-388040/33.
 XX
 XX Immunogenic polypeptide from hepatitis B surface antigen - useful
 PT in, e.g. vaccine against hepatitis B virus or hepatitis delta virus
 PT infection
 XX
 XX Example 3; Page 35; 71pp; English.
 PS
 XX The invention relates to an immunogenic peptide derived from hepatitis B
 CC surface antigen (HBsAg) which competes with the hepatitis B surface
 CC antigen/annexin V interaction or which binds a compound or antibody
 CC competing with the hepatitis B surface antigen/annexin V interaction.
 CC Also claimed are: (1) a combination of the immunogenic peptide and a
 CC negatively charged phospholipid; (2) a peptide composition comprising
 CC the immunogenic peptide; (3) a vaccine comprising the immunogenic peptide
 CC as an active substance; (4) antibodies which specifically bind to the
 CC peptide and inhibit binding of HBsAg to annexin V, and (5) a therapeutic
 CC composition comprising as an active substance the antibodies of (4).
 CC The vaccine of (3), and the therapeutic composition of (5), can be used
 CC as an inoculum to vaccinate humans against an infection with hepatitis
 CC B and/or hepatitis delta virus. The immunogenic peptide can be used in a
 CC method to detect antibodies which are capable of competing with the
 CC hepatitis B and/or hepatitis delta virus surface antigen/annexin V
 CC interaction. The immunogenic peptide can also be used to screen for
 CC drugs which block the binding between annexin V and the peptide, and as
 CC a therapeutic to treat humans infected with hepatitis B virus and/or
 CC hepatitis delta virus. The present sequence represents one of the
 CC peptide fragments derived from HBsAg which were synthesised to map the
 CC annexin V-binding site on HBsAg.
 XX
 XX Sequence 23 AA;

Query Match 25.7%; Score 34.5; DB 19; Length 23;
 Best Local Similarity 44.4%; Pred. No. 2.8e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
 QY 1 PCAGTFSNTSTSDICR 18
 I III :::I
 Db 1 pllpgt---sttstgpc 15

RESULT 12
 AAU05353
 ID AAU05353 standard; peptide; 20 AA.
 XX
 XX AAU05353;
 AC
 XX
 XX 24-OCT-2001 (first entry)
 DT
 XX
 XX R1 and R2 peptide #47 useful as erythropoietin receptor agonist.
 DE
 XX
 XX Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
 KW renal failure; anaemia; chronic inflammatory disease;
 KW autoimmune disease; malignancy; red blood count.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200138342-A2.
 PN
 XX
 XX 31-MAY-2001.
 PD
 XX
 XX 24-NOV-2000; 2000WO-US32224.
 PF
 XX
 XX 24-NOV-1999; 99US-0449064.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Balu P;
 PI
 XX

DR WPI; 2001-417749/44.

XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by

PT binding linking group with functional groups as initiation sites for

PT peptide synthesis to support and synthesizing peptide segments.

XX Disclosure; Fig 1; 43pp; English.

XX The present sequence for potential R1 and R2 peptide #47 can be used

CC to form a peptide dimer that binds and activates the erythropoietin

CC receptor (EPO-R). Various possible peptide sequences for R1 and R2

CC (AAU05301-AAU05393) are described in the present invention. Also

CC described is a method for synthesizing such peptide dimers which

CC act as EPO-R agonists. The method is useful for synthesizing peptide

CC dimers which are useful, in vitro, as tools for understanding the

CC biological role of EPO, in the development of other compounds that bind

CC to EPO-R, as commercial research reagents for various medical research

CC and diagnostic applications, for detecting EPO receptors on living

CC cells, for treatment of disorders associated with a deficiency of EPO,

CC such as end-stage renal failure/dialysis, anaemia associated with AIDS

CC and chronic inflammatory diseases, autoimmune diseases and malignancies,

CC and for boosting the red blood count of a patient prior to surgery.

XX Sequence 20 AA:

Query Match 25.4%; Score 34; DB 22; Length 20;

Best Local Similarity 57.1%; Pred. No. 2.9e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 14 TDICRPH 20

Db 12 tbverpn 18

RESULT 13

AAB23019

ID AAB23019 standard; peptide; 20 AA.

XX AC AAB23019;

XX 16-JAN-2001 (first entry)

XX Human APC protein 20 aa repeat #4 (1643-1662).

XX APC gene; Adenomatous Polyposis Coli gene; human; chromosome 5q21;

XX familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS;

XX sporadic tumour; adenoma; carcinoma; cancer; lung; breast; colon; rectum;

XX bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma;

XX tumour suppressor; anti-APC antibody; detection; diagnosis; prognosis;

XX genetic predisposition; drug screening; DP2.5; repeat region.

XX Homo sapiens.

XX US6114124-A.

XX 05-SEP-2000.

XX 25-MAY-1995; 95US-0450582.

XX 16-JAN-1991; 91GB-0000962.

XX 16-JAN-1991; 91GB-0000963.

XX 16-JAN-1991; 91GB-0000974.

XX 16-JAN-1991; 91GB-0000975.

XX 08-AUG-1991; 91US-0741940.

XX 12-AUG-1994; 94US-0289548.

XX (ICIL) IMPERIAL CHEM IND PLC.

XX (UYJO) UNIV JOHNS HOPKINS.

XX (UTAH) UNIV UTAH.

XX (CANC-) CANCER INST.

XX Carlson M, Groden J, Joslyn G, Kinzler K, Markham AF, Anand R;

PI Albertsen H, White RL, Thliveris A, Nakamura Y, Vogelstein B;

XX Hedge PJ;

XX WPI; 2000-565003/52.

XX Detecting Adenomatous Polyposis Coli (APC) protein in a sample for

PT diagnosing cancers, involves contacting the sample with antibodies that

PT specifically bind to APC protein and detecting the complex formed.

XX Example 15; Column 33-34; 125pp; English.

XX The invention relates to a novel method for detecting Adenomatous

CC Polyposis Coli (APC) protein in a sample. The method involves

CC contacting the sample with antibodies which specifically binds to the

CC 2843 amino acid form of the human APC protein, or to a mutant APC

CC protein, and detecting an APC-antibody complex. Mutations in the APC

CC gene play a role in tumorigenesis, indicating that it is a tumour

CC suppressor gene. It is located on chromosome 5q21, which corresponds to

CC the FAP (familial adenomatous polyposis) locus. FAP is an autosomal

CC dominant inherited disease in which affected individuals develop

CC hundreds to thousands of adenomatous polyps in the colon and rectum,

CC some of which progress to malignancy. The FAP locus is often found to

CC be deleted in sporadic (i.e., non-familial) adenomas and carcinomas, and

CC chromosome 5q deletions have also been observed in tumours of the lung,

CC breast, colon, rectum, bladder, liver, sarcomas, stomach, and prostate,

CC and in leukaemias and lymphomas. Although the FAP locus contains

CC several other genes such as FER, TBI, TB2, and MCC, it is thought that

CC mutations in the APC gene play a key role in the development of FAP and

CC sporadic tumours. The method is useful for detecting APC protein and its

CC mutant forms in foetal tissue, placental tissue, amniotic fluid, blood,

CC serum or a tumour sample. The method is useful for diagnosing or

CC prognosing neoplastic tissue, for detecting a genetic predisposition to

CC cancer, for detecting germline and somatic alteration of wild-type APC

CC genes, and for testing therapeutic agents for the ability to suppress

CC tumours. Sequences AAB23016-B23022 represent seven 20 amino acid repeats

CC that are semiregularly spaced in the human APC protein.

XX Sequence 20 AA:

Query Match 25.0%; Score 33.5; DB 21; Length 20;

Best Local Similarity 44.4%; Pred. No. 3.4e+02;

Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 CAPGT---FSNTTSSTDI 16

Db 2 cvegtptinfstatslsdi 19

RESULT 14

AAY20893

ID AAY20893 standard; Protein; 15 AA.

XX AC AAY20893;

XX 22-JUL-1999 (first entry)

XX Human presenilin I mutant protein fragment 39.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;

XX frameshift mutation; age-related disease; neurodegenerative disorder;

XX Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;

XX Huntington's disease; multiple sclerosis; alcoholic liver disease;

XX diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;

XX ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-W;

XX neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;

XX glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;

XX bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;

XX high mobility group protein-C; neuroendocrine specific protein A.

XX Synthetic.

XX Homo sapiens.

PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF
XX 02-APR-1998; 98WO-IB00705.
XX
PR 10-APR-1997; 97US-0043163.
XX
PA (UYUT-) RIJKSNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75761.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
PS Disclosure; Figure 10; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC use of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin-B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin 1, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HspF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A.
XX
SQ Sequence 15 AA;

Query Match 24.6%; Score 33; DB 19; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CARGTF 7
Db | | | |
4 ccpgtf 9

RESULT 15
AAR75932
ID AAR75932 standard; Protein; 16 AA.
XX
AC AAR75932;
XX
DT 24-FEB-1996 (first entry)
XX
DE Dextranase N-terminal sequence.
XX
KW Dextranase; thermostable enzyme; dextran hydrolysis; sugar.
XX
OS Penicillium minioluteum HI-4.
XX
PN EP663443-A1.
XX
PD 19-JUL-1995.

XX
PF 13-DEC-1994; 94EP-0203614.
XX
PR 14-DEC-1993; 93CU-0000115.
XX
PA (LINGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX
PI Delgado Boada JM, Campana HR, Curbelo DM, Jimenez ER;
PI Patron CF, Cremata Alvarez JA, Garcia Fernandez R;
PI Garcia Garcia BM, Gonzalez Martinez ME, Herrera Martinez LS;
PI Margollez Clark E, Morera Cordova V, Raices Perez-Castaneda MR;
XX
DR WPI; 1995-247530/33.
XX
PT Nucleotide sequence encoding Penicillin minioluteum dextranase -
PT useful for the high-level industrial prodn. of dextranase.
XX
PS Example 2; Page 7; 29pp; English.
XX
CC The N-terminal region of P. minioluteum dextranase was sequenced
CC using the Edman degradation method. Dextranase may be secreted as
CC a recombinant protein by the transformed host, Pichia pastoris.
CC The recombinant enzyme has higher thermal stability than the natural
CC P. minioluteum enzyme (specifically an optimum temp. of 55-60 deg
CC and a half-life of 7.6 hr at 50 deg), and it can be used in the sugar
CC industry for sugarcane juice dextran hydrolysis.
XX
SQ Sequence 16 AA;

Query Match 24.6%; Score 33; DB 16; Length 16;
Best Local Similarity 46.2%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 GTFSNNTSSTDIC 17
Db | | | | |
2 gttntnhtcgadfc 14

Search completed: February 12, 2002, 13:03:52
Job time: 192 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 13:02:40 ; Search time 12.45 seconds
(without alignments)
41.572 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_185

Perfect score: 134

Sequence: 1 PCAGTFSNTTSTSDICRPHQIC 23

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Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 119836

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	53.7	15	1 US-08-221-583-45	Sequence 45, Appl
2	72	53.7	15	1 US-08-221-583-46	Sequence 46, Appl
3	72	53.7	15	5 PCT-US95-04018-45	Sequence 45, Appl
4	72	53.7	15	5 PCT-US95-04018-46	Sequence 46, Appl
5	71	53.0	15	1 US-08-221-583-44	Sequence 44, Appl
6	71	53.0	15	5 PCT-US95-04018-44	Sequence 44, Appl
7	57	42.5	15	1 US-08-221-583-47	Sequence 47, Appl
8	57	42.5	15	5 PCT-US95-04018-47	Sequence 47, Appl
9	48	35.8	20	2 US-08-126-016-24	Sequence 24, Appl
10	44	32.8	15	1 US-08-221-583-48	Sequence 48, Appl
11	44	32.8	15	5 PCT-US95-04018-48	Sequence 48, Appl
12	39	29.1	23	3 US-09-101-146-58	Sequence 58, Appl
13	33	24.6	16	1 US-08-354-618-3	Sequence 3, Appl
14	33	24.6	20	2 US-08-934-915-141	Sequence 141, Appl
15	32	23.9	15	1 US-08-493-092-4	Sequence 4, Appl
16	32	23.9	15	1 US-08-508-836A-4	Sequence 4, Appl
17	32	23.9	15	2 US-08-629-001A-4	Sequence 4, Appl
18	32	23.9	15	4 US-08-642-274D-4	Sequence 4, Appl
19	32	23.9	15	4 US-08-952-127-4	Sequence 4, Appl
20	32	23.9	15	4 US-08-952-014C-4	Sequence 4, Appl
21	32	23.9	22	1 US-08-484-635-178	Sequence 178, Appl
22	32	23.9	22	2 US-08-484-631-178	Sequence 178, Appl
23	32	23.9	22	2 US-08-827-570-178	Sequence 178, Appl
24	31.5	23.5	20	1 US-08-318-193-63	Sequence 63, Appl
25	31	23.1	18	4 US-09-461-697-449	Sequence 449, Appl
26	31	23.1	18	6 5217891-2	Patent No. 5217891
27	31	23.1	20	2 US-08-934-915-78	Sequence 78, Appl

28 31 23.1 20 4 US-08-612-973-83 Sequence 83, Appl
29 31 23.1 20 4 US-08-927-597-83 Sequence 83, Appl
30 30 22.4 18 1 US-08-323-531-8 Sequence 8, Appl
31 30 22.4 18 1 US-08-198-094-8 Sequence 8, Appl
32 30 22.4 18 4 US-08-107-794A-8 Sequence 8, Appl
33 30 22.4 18 5 PCT-US93-07424-8 Sequence 8, Appl
34 30 22.4 18 5 PCT-US95-02087-8 Sequence 8, Appl
35 30 22.4 19 1 US-08-484-635-244 Sequence 244, App
36 30 22.4 19 2 US-08-484-631-244 Sequence 244, App
37 30 22.4 19 2 US-08-827-570-244 Sequence 244, App
38 29.5 22.0 16 1 US-08-574-763-7 Sequence 7, Appl
39 29 21.6 6 4 US-08-750-142B-20 Sequence 20, Appl
40 29 21.6 9 1 US-08-054-860-14 Sequence 14, Appl
41 29 21.6 9 3 US-08-442-378-14 Sequence 14, Appl
42 29 21.6 12 4 US-08-602-999A-280 Sequence 280, App
43 29 21.6 15 1 US-08-221-583-49 Sequence 49, Appl
44 29 21.6 15 4 US-08-602-999A-315 Sequence 315, App
45 29 21.6 15 5 PCT-US95-04018-49 Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-221-583-45
; Sequence 45, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-45

Query Match 53.7%; Score 72; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00083;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GTFSTNTSSTDICRP 19
|||||

Db 1 GTFSTNTSSTDIARP 15
|||||

RESULT 2

US-08-221-583-46
; Sequence 46, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-46

Query Match 53.7%; Score 72; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00083;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SNTTSTSDICRPHQI 22
| | | | | | | | | | | | | | | | | |
Db 1 SNTTSTSDIARPHQI 15

RESULT 3
PCT-US95-04018-45
; Sequence 45, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSER: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-45

Query Match 53.7%; Score 72; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00083;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GTFSNTTSTSDICRP 19
| | | | | | | | | | | | | | | | | |
Db 1 GTFSNTTSTSDIARP 15

RESULT 4
PCT-US95-04018-46
; Sequence 46, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSER: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-46

Query Match 53.7%; Score 72; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00083;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 SNTTSSDTCRPHQI 22
Db 1 SNTTSSDTCRPHQI 15

RESULT 5
US-08-221-583-44

Sequence 44, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-44

Query Match 53.0%; Score 71; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APGTFSTNTSSTDI 16
Db 2 APGTFSTNTSSTDI 15

RESULT 6

PCT-US95-04018-44
Sequence 44, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-44

Query Match 53.0%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APGTFSTNTSSTDI 16
Db 2 APGTFSTNTSSTDI 15

RESULT 7

US-08-221-583-47
Sequence 47, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
STREET: One Liberty Place 46th Floor
CITY: Philadelphia

```
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctoMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-221-583-47

Query Match 42.5%; Score 57; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.082;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TSSTDICRPHQI 22
Db 1 TSSTDICRPHQI 12

RESULT 8
PCT-US95-04018-47
; Sequence 47, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-47

Query Match 42.5%; Score 57; DB 5; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.082;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TSSTDICRPHQI 22
Db 1 TSSTDICRPHQI 12

RESULT 9
US-08-126-016-24
; Sequence 24, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID
; APPLICANT: NOPAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, CORD
; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625668
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-126-016-24

Query Match 35.8%; Score 48; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PCAPGTF 8
| | | | | | | |
Db 12 PCAPGTF 19

RESULT 10

US-08-221-583-48
; Sequence 48, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221.583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-48

Query Match 32.8%; Score 44; DB 1; Length 15;
Best Local Similarity 88.9%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TDICRPHQI 22
| | | | | | | |
Db 1 TDIARPHQI 9

RESULT 11

PCT-US95-04018-48
; Sequence 48, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-48

Query Match 32.8%; Score 44; DB 5; Length 15;
Best Local Similarity 88.9%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TDICRPHQI 22
| | | | | | | |
Db 1 TDIARPHQI 9

RESULT 12

US-09-101-146-58
; Sequence 58, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998

CLASSIFICATION: 435
PRIOR APPLICATION DATA: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-101-146-58

Query Match 29.1%; Score 39; DB 3; Length 23;
Best Local Similarity 43.8%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 CAPGTFSTNTSSDTC 17
||| : | : |
Db 4 CAAGTTTGATGTATC 19

RESULT 13
US-08-354-618-3
; Sequence 3, Application US/08354618
; Patent No. 5637491
; GENERAL INFORMATION:
; APPLICANT: Campana, Hernan Roca
; APPLICANT: Garcia, Blanca Maria Garcia
; APPLICANT: Clark, Emilio Margollez
; APPLICANT: Curbelo, Dania Mateu
; APPLICANT: Boada, Julio Marcos Delgado
; APPLICANT: Martinez, Luis S. Herrera
; APPLICANT: Alvarez, Jos Alberto Cremata
; APPLICANT: Perez-Casta eda, Manuel Rafael Raices
; APPLICANT: Martinez, Maria Elena Gonz lez
; APPLICANT: Jim nez, Efraim Rodriguez
; TITLE OF INVENTION: Dextranase enzyme, method for its
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ronald J. Baron
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.0 version B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,618
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 115/93
; FILING DATE: 14-December-1993
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

US-08-354-618-3

Query Match 24.6%; Score 33; DB 1; Length 16;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 GTFSTNTSSDTC 17
|| : || : |
Db 2 GTTNTHCAGDFC 14

RESULT 14
US-08-934-915-141
; Sequence 141, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-141

Query Match 24.6%; Score 33; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 SNTTSSTDCIRPH 20
||| : | : |
Db 7 SNEVSSPEIRQH 19

RESULT 15
US-08-493-092-4
; Sequence 4, Application US/08493092

; Patent No., 5728807
; GENERAL INFORMATION:
; APPLICANT: Shiloh, Yosef
; APPLICANT: Taglie, Danilo A.
; APPLICANT: Collins, Francis S.
; TITLE OF INVENTION: Ataxia-Telangiectasia Gene
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/493,092
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-310 (TAV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-493-092-4

Query Match 23.9%; Score 32; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 8 SNTTSSTDIC 17
I : |||:
Db 6 SSASQSTDLC 15

Search completed: February 12, 2002, 13:04:30
Job time: 110 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	38.5	17.8	37	2	G49050	T-cell surface gly	
2	38	17.6	33	2	A37479	huentoxin-I - Chi	
3	34	15.7	37	2	S58261	hypothetical prote	
4	33.5	15.5	39	2	A05323	phospholipase A2 (
5	33	15.3	39	2	G82613	hypothetical prote	
6	32.5	15.0	35	2	A09059	agelatin - funnel-	
7	32	14.8	30	2	A32977	delta-endotoxin -	
8	31	14.4	30	2	A42865	Ca2+/calmodulin-de	
9	31	14.4	30	2	S70343	napin large chain	
10	31	14.4	34	2	E9410	t-complex polypept	
11	31	14.4	38	2	A60716	somatotropin intro	
12	30.5	14.1	38	2	A48158	phormone precursor	
13	30	13.9	18	2	B49048	T-cell receptor be	
14	30	13.9	26	2	S28994	antifungal protein	
15	30	13.9	29	2	G61233	conceptus protein	
16	30	13.9	35	2	A39830	dentin matrix, inc	
17	30	13.9	38	2	A45495	beta-defensin-1 -	
18	29	13.4	13	2	S47381	T-cell antigen rec	
19	29	13.4	16	2	S38292	30K allergen - rye	
20	29	13.4	17	2	A00317	glucagon-like pept	
21	29	13.4	21	2	I34351	gene HEXA protein	
22	29	13.4	22	2	A39269	LX-1 tumor antigen	
23	29	13.4	24	2	S08293	lectin - sunn hemp	
24	29	13.4	26	2	B42865	Ca2+/calmodulin-de	
25	29	13.4	31	2	S53233	gene x protein - h	
26	29	13.4	32	2	I48415	heat shock factor	
27	29	13.4	34	2	D81044	hypothetical prote	
28	28	13.0	18	1	A58589	alpha-conotoxin EI	
29	28	13.0	23	2	S60565	homeodomain protei	

A37479
 huwentoxin-I - Chinese bird spider
 C:Species: *Scenecosmia huwena* (Chinese bird spider)
 C:Date: 18-Mar-1994 #sequence_revision 07-Oct-1994 #text
 C:Accession: A37479; JG1089
 R:LiJiang, S.P.; Zhang, D.Y.; Pan, X.; Chen, Q.; Zhou, P.A.
 T:Toxicol 31, 969-978, 1993
 A:Title: Properties and amino acid sequence of huwentoxin
 A:Reference number: A37479; MUID:94024948

A:Residues: 1-33 <L12>
R:liang, S.P.; Jong, X.; Luo, J.C.; Jing, H.; Gu, X.C.
Acta Sci. Natur. Univ. Pekin. 29, 668-674, 1993
A:Title: Secondary structure study of huwentoxin-I, a
A:Reference number: JCI089
A:Accession: JCI089
A:Molecule type: protein
A:Residues: 1-33 <L12>
C:Comment: This peptide is the major active protein co

C:Keywords: presynaptic neurotoxin: venom
F:2-17,9-22,16-29/Disulfide bonds: #status experimental

Query Match 17.6%; Score 38; DB 2; Length 33;
Best Local Similarity 30.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 5 GTFSNTSTSDICRPHQICN 24
| | | : | | | |
Db 4 GVFDACPGKNECCPNRVCs 23

RESULT 3
S68261

hypothetical protein gadd7.2 - long-tailed hamster
C:Species: Cricetus longicaudatus (long-tailed hamster)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68261
R:Hollander, M.C.; Alamo, I.; Fornace Jr., A.J.
Nucleic Acids Res. 24, 1589-1593, 1996
A:Title: A novel DNA damage-inducible transcript, gadd7, inhibits cell growth, but lacks
A:Reference number: S68260; MUID:96211359
A:Accession: S68261
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-37 <HOL>
A:Cross-references: EMBL:L40430

Query Match 15.7%; Score 34; DB 2; Length 37;
Best Local Similarity 60.0%; Pred. No. 7.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 23 CNVVAIPGNA 32
| | | | | | | |
Db 10 CTVTRAPGNA 19

RESULT 4
A05323

phospholipase A2 (EC 3.1.1.4) - Mexican beaded lizard (fragment)
N:Alternate names: phosphatidylcholine 2-acylhydrolase
C:Species: Heloderma horridum (Mexican beaded lizard)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-Apr-1995
C:Accession: A05323
R:Sosa, B.P.; Alagon, A.C.; Martin, B.M.; Possani, L.D.
Biochemistry 25, 2927-2933, 1986
A:Reference number: A05323; MUID:86243292
A:Note: H. h. horridum
A:Accession: A05323
A:Molecule type: protein
A:Residues: 1-39 <SOS>

C:Comment: Phospholipases A2 catalyze the calcium-dependent hydrolysis of the 2-acyl glycerol
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; venom

Query Match 15.5%; Score 33.5; DB 2; Length 39;
Best Local Similarity 31.0%; Pred. No. 9.6e+02;
Matches 9; Conservative 3; Mismatches 10; Indels 7; Gaps 2;

QY 2 CAPGTFSN-----TTSSTDI-CRPHQIC 23
| | | : | | | | | | | |
Db 11 CGAGNAADYSQLGTEKDTDMCCRDHDC 39

RESULT 5
G82613

hypothetical protein Xf1988 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: G82613

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82613
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-39 <SIM>
A:Cross-references: GB:AE004018; GB:AE003849; NID:g9107093; PIDN:AAF84790.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreras-Neto, E.; Docena, C.; El-Dorri, H.; Facincanli, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurmae, E.E.; L. chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1988

Query Match 15.3%; Score 33; DB 2; Length 39;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 6 TFSNTTSTSDICRPHO 21
: | | | | | : | | :
Db 24 SLSKVTVSADVMRAHR 39

RESULT 6
A60959

agelenin - funnel-weaving spider (Agelena opulenta)
C:Species: Agelena opulenta
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 24-Feb-1994
C:Accession: A60959
R:Hagiwara, K.; Sakai, T.; Miwa, A.; Kawai, N.; Nakajima, T.
Biomed. Res. 11, 181-186, 1990
A:Title: Complete amino acid sequence of a new type of neurotoxin from the venom of
A:Reference number: A60959
A:Accession: A60959
A:Molecule type: protein
A:Residues: 1-35 <HAG>
C:Keywords: calcium channel inhibitor; presynaptic neurotoxin; venom

Query Match 15.0%; Score 32.5; DB 2; Length 35;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 17 CRPH-QTCNVVAIP 29
| | | : | | : |
Db 3 CLPHNRCNALSGP 16

RESULT 7
A22977

delta-endotoxin - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 07-Feb-1997
C:Accession: A22977
R:Armstrong, J.L.; Rohrmann, G.F.; Beaudreau, G.S.
J. Bacteriol. 161, 39-46, 1985
A:Reference number: A22977; MUID:85104736
A:Accession: A22977

C:Accession: A48158
 R:Moore, T.D.; Edman, J.C.
 Mol. Cell. Biol. 13, 1962-1970, 1993
 A:Title: The alpha-mating type locus of *Cryptococcus neoformans* contains a peptide phage-coded gene
 A:Reference number: A48158; MUID:93180845
 A:Accession: A48158
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-38 <MOO>
 A:Note: sequence inconsistent with nucleotide translation

conceptus [Protein 5 - cat (fragment)
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 C:Accession: C61233
 R:Thatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazzer, F.W.; Sisum, W.; Randal, S.

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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:56:25 ; Search time 10.18 Seconds
(without alignments)
140.464 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_201

Perfect score: 216

Sequence: 1 PCAPGTFSTNTSSDTCRPHQICNVAILPGNSMDAVCT 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 2657

Minimum DB seq length: 0

Maximum DB seq length: 39

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	17.6	33	1 TXHL_SELHU	P56676 selenocosmi
2	37.5	17.4	37	1 TXJC_HADVE	P82228 hadronyche
3	37	17.1	36	1 TXJA_HADVE	P82227 hadronyche
4	34	15.7	36	1 TXJB_HADVE	P82226 hadronyche
5	33.5	15.5	39	1 PA2_HELHO	P04362 heloderma h
6	32.5	15.0	35	1 TXAG_AGEOP	P31328 agelena opu
7	31	14.4	28	1 PPOX_BOVIN	P56602 bos taurus
8	31	14.4	30	1 CY01_VIOOD	P82230 viola odora
9	30	13.9	31	1 CYLA_PSYLO	P56872 psychotria
10	30	13.9	38	1 BD01_BOVIN	P46159 bos taurus
11	29	13.4	15	1 DIDH_PSESP	P80701 pseudomonas
12	29	13.4	24	1 LEC_CROJU	P16352 crotalaria
13	29	13.4	34	1 RR2_OCHNE	Q40606 ochrosphaer
14	28	13.0	18	1 CXAL_CONER	P50382 conus ermin
15	28	13.0	29	1 GLUC_PLAFE	P23062 platichthys
16	28	13.0	30	1 IT11_LAGLE	P26771 lagenaria l
17	28	13.0	30	1 ITR1_CITLA	P11969 citrullus l
18	28	13.0	36	1 GLU1_ORENI	P81026 oreochromis
19	27.5	12.7	31	1 CXD6_CONNI	P56710 conus nigro
20	27	12.5	22	1 CXM1_CONGE	P01323 conus geogr
21	27	12.5	23	1 AFP2_BRANA	P30226 brassica na
22	27	12.5	24	1 RS13_THETH	P80377 thermus aqu
23	27	12.5	25	1 AND1_ANDAU	P56684 androctonus
24	27	12.5	27	1 AFP1_BRARA	P30227 brassica ra
25	27	12.5	28	1 ETX2_BACCE	P80368 bacillus ce
26	27	12.5	28	1 PA2C_PSEPO	P20260 pseudechis
27	27	12.5	30	1 VPU_HVISC	P05948 human immun
28	27	12.5	30	1 LPTV_ECOLI	P30361 escherichia
29	26.5	12.3	32	1 IAPP_SHEEP	Q28605 ovis aries
30	26	12.0	38	1 NLFX_WHEAT	P39085 triticum ae
31	26	12.0	30	1 GLUM_ANGAN	P41521 anguilla ae
32	26	12.0	30	1 ITRI_MOMCH	P10294 momordica c
33	26	12.0	33	1 VTL1_RAT	P58200 rattus norv

34	26	12.0	34	1 DEF2_RABIT	P07468 oryctolagus
35	26	12.0	37	1 RL36_MYCPN	P52864 mycoplasma
36	25.5	11.8	23	1 CP23_SPOER	P56683 spodoptera
37	25.5	11.8	23	1 PAP2_SPOEX	P30256 spodoptera
38	25.5	11.8	23	1 PAP3_SPOEX	P30257 spodoptera
39	25.5	11.8	32	1 CAPP_METEX	Q49136 methylobact
40	25.5	11.8	34	1 TX1_SCOGR	P56855 scodra grls
41	25.5	11.8	37	1 RL36_LEPIN	O9kd13 leptospira
42	25.5	11.8	37	1 RL36_VIRCH	P78001 vibrio chol
43	25.5	11.8	37	1 TXM2_AGEAP	P11058 agelenopsis
44	25.5	11.8	38	1 BD08_BOVIN	P46166 bos taurus
45	25	11.6	11	1 TKNA_ONCMY	P28499 oncorhynch

ALIGNMENTS

RESULT 1

ID	TXHL_SELHU	STANDARD;	PRT;	33 AA.
AC	P56676; Q9NJC2;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	HUWENTOXIN-I (HWTX-I)			
OS	Selenocosmia huwena (Chinese bird spider).			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;			
OC	Mygalomorphae; Theraphosidae; Selenocosmia.			
OX	NCBI_TaxID=29017;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=94024948; PubMed=8212049;			
RA	Liang S.-P., Zhang D.-Y., Pan X., Chen Q., Zhou P.-A.;			
RT	"Properties and amino acid sequence of huwentoxin-I, a neurotoxin			
RT	purified from the venom of the Chinese bird spider Selenocosmia			
RT	huwena.";			
RL	Toxicon 31:969-978(1993).			
RN	[2]			
RP	SEQUENCE OF 1-32 FROM N.A.			
RC	STRAIN=Huwen;			
RA	Li M., Zhou Z., Liang S.;			
RT	"Huwentoxin-I (HWTX-I) peptide cDNA sequence.";			
RT	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	STRUCTURE BY NMR.			
RC	TISSUE=Venom;			
RX	MEDLINE=97408601; PubMed=9263120;			
RA	Qu Y.-X., Liang S.-P., Ding J., Liu X.-C., Zhang R.-J., Gu X.-C.;			
RT	"Proton nuclear magnetic resonance studies on huwentoxin-I from the			
RT	venom of the spider Selenocosmia huwena: 2. Three-dimensional			
RT	structure in solution.";			
RL	J. Protein Chem. 16:565-574(1997).			
RN	[4]			
RP	DISULFIDE BONDS.			
RC	TISSUE=Venom;			
RX	MEDLINE=94183409; PubMed=8136023;			
RA	Zhang D.-Y., Liang S.-P.;			
RT	"Assignment of the three disulfide bridges of huwentoxin-I, a			
RT	neurotoxin from the spider Selenocosmia huwena.";			
RL	J. Protein Chem. 12:735-740(1993).			
RN	[5]			
RP	CHARACTERIZATION.			
RX	MEDLINE=97179771; PubMed=9028007;			
RA	Zhou P.-A., Xie X.-J., Li M., Yang D.-M., Xie Z.-P., Zong X.,			
RT	Liang S.-P.;			
RT	"Blockade of neuromuscular transmission by huwentoxin-I, purified from			
RT	the venom of the Chinese bird spider Selenocosmia huwena.";			
RL	Toxicon 35:39-45(1997).			
CC	-I- FUNCTION: LETHAL NEUROTOXIN. BINDS TO THE NICOTINIC ACETYLCHOLINE			
CC	RECEPTOR. BLOCKS NEUROMUSCULAR TRANSMISSION.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; AF157504; AAF25774.1; -
 DR PDB; 1QK6; 20-AUG-99.
 KW Venom: Neurotoxin; Postsynaptic neurotoxin; 3D-structure.
 FT DISULFID 2 17
 FT DISULFID 9 22
 FT DISULFID 16 29
 SQ SEQUENCE 33 AA; 3756 MW; 1CCE219FD6D31F11 CRC64;

Query Match 17.6%; Score 38; DB 1; Length 33;
 Best Local Similarity 30.0%; Pred. No. 70;
 Matches 6; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 5 GTFSTNTSSDTCRPHOICN 24
 Db 4 GVFDCTPGRNECCPNRVCS 23

RESULT 2
 TXJC_HADVE STANDARD; PRT; 37 AA.
 AC P82228;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE J-ATRACOTOXIN-HV1C (J-ACTX-HV1C).
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
 OS versutus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_TaxID=6904;
 RN [1]
 RP SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
 RC TISSUE=Venom gland;
 RX MEDLINE=20343014; PubMed=10881200;
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
 RA Nicholson G.M., Christie M.J., King G.F.;
 RT "Discovery and characterization of a family of insecticidal
 RT neurotoxins with a rare vicinal disulfide bridge."
 RL Nat. Struct. Biol. 7:505-513(2000).
 CC -!- FUNCTION: INSECTICIDAL NEUROTOXIN.
 CC Venom; Toxin; Neurotoxin; 3D-structure.
 KW DISULFID 3 17
 FT DISULFID 10 22
 FT DISULFID 13 14
 FT DISULFID 16 32
 SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;

Query Match 17.4%; Score 37.5; DB 1; Length 37;
 Best Local Similarity 42.1%; Pred. No. 92;
 Matches 8; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 PCAPGTFSNTTSS-TDCCR 18
 Db 15 PCCPGTSCKAESNGSVYCR 33

RESULT 3
 TXJA_HADVE STANDARD; PRT; 36 AA.
 AC P82227;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE J-ATRACOTOXIN-HV1A (J-ACTX-HV1A).
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
 OS versutus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_TaxID=6904;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom gland;
 RX MEDLINE=20343014; PubMed=10881200;
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
 RA Nicholson G.M., Christie M.J., King G.F.;
 RT "Discovery and characterization of a family of insecticidal
 RT neurotoxins with a rare vicinal disulfide bridge."
 RL Nat. Struct. Biol. 7:505-513(2000).
 CC -!- FUNCTION: INSECTICIDAL NEUROTOXIN.
 CC Venom; Toxin; Neurotoxin.
 KW DISULFID 3 17
 FT DISULFID 10 22
 FT DISULFID 13 14
 FT DISULFID 16 33
 SQ SEQUENCE 36 AA; 3685 MW; D1598B2560BFE997 CRC64;

Query Match 17.1%; Score 37; DB 1; Length 36;
 Best Local Similarity 40.0%; Pred. No. 1e+02;
 Matches 8; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

QY 1 PCAPGTFSNTTSSDI--CR 18
 Db 15 PCCPGTSCQGPESNGVYCR 34

RESULT 4
 TXJB_HADVE STANDARD; PRT; 36 AA.
 AC P82226;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE J-ATRACOTOXIN-HV1B (J-ACTX-HV1B).
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
 OS versutus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_TaxID=6904;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom gland;
 RX MEDLINE=20343014; PubMed=10881200;
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,
 RA Nicholson G.M., Christie M.J., King G.F.;
 RT "Discovery and characterization of a family of insecticidal
 RT neurotoxins with a rare vicinal disulfide bridge."
 RL Nat. Struct. Biol. 7:505-513(2000).
 CC -!- FUNCTION: INSECTICIDAL NEUROTOXIN.
 CC Venom; Toxin; Neurotoxin.
 KW DISULFID 3 17
 FT DISULFID 10 22
 FT DISULFID 13 14
 FT DISULFID 16 33
 SQ SEQUENCE 36 AA; 3651 MW; D23A442560B89997 CRC64;

Query Match 15.7%; Score 34; DB 1; Length 36;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PCAPGT 6
 Db 15 PCCPGT 20

```

RESULT 5
PA2_HELHO STANDARD; PRT; 39 AA.
AC P04362;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)
DE (FRAGMENT).
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=66243292; PubMed=3087412;
RA Sosa B.P., Alagon A.C., Martin B.M., Possani L.D.;
RT "Biochemical characterization of the phospholipase A2 purified from
RT the venom of the Mexican beaded lizard (Heloderma horridum
RT Wiegmann).";
RL Biochemistry 25:2927-2933(1986).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC PIR: A05323; A05323.
DR HSP: P00630; IPOC.
DR InterPro: IPR001211; PLP_A2.
DR PROSITE: PS00119; PA2_ASP; PARTIAL.
DR PROSITE: PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Venom.
FT ACT_SITE 36 36 BY SIMILARITY.
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4179 MW; 8F9BC6B5DBF603E CRC64;

Query Match 15.5%; Score 33.5; DB 1; Length 39;
Best Local Similarity 31.0%; Pred. No. 3 3e+02;
Matches 9; Conservative 3; Mismatches 10; Indels 7; Gaps 2;

QY 2 CAPGTFSTN-----TTSSTDI-CRPHQIC 23
Db 11 CGAGNAASDYSQLGTEKDTDMCCRDHDC 39

RESULT 6
TXAG_AGEOP STANDARD; PRT; 35 AA.
AC P31328;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE AGELENIN.
OS Agelena opulenta (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Enelegynae; Agelenidae; Agelena.
OX NCBI_TaxID=29934;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Hagiwara K., Sakai T., Miwa A., Kawai N., Nakajima T.;
RT "Complete amino acid sequence of a new type of neurotoxin from the
RT venom of the spider, Agelena opulenta.";
RL Biomed. Res. 11:181-186(1990).
RN [2]
RP DISULFIDE BONDS, AND AMIDATION.
RC TISSUE=Venom;
RA Hagiwara K., Inui T., Nakajima K., Kimura T., Kitada C., Fujino M.,
RA Sakakibara S., Nakajima T.;
RT "Agelenin, a spider neurotoxin: determination of the C-terminus as

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RT amide form, and investigation of the disulfide bond arrangement.";
RL Biomed. Res. 12:357-363(1991).
RN [3]
RP SYNTHESIS, DISULFIDE BONDS, AND AMIDATION.
RC TISSUE=Venom;
RX MEDLINE=93043890; PubMed=1421801;
RA Inui T., Hagiwara K., Nakajima K., Kimura T., Nakajima T.,
RA Sakakibara S.;
RT "Synthesis and disulfide structure determination of agelenin:
RT identification of the carboxy-terminus as an amide form.";
RL Pept. Res. 5:140-144(1992).
CC -1- FUNCTION: SUPPRESSES THE EXCITATORY POSTSYNAPTIC POTENTIALS
CC POSSIBLY BY BLOCKING THE PRESYNAPTIC CALCIUM CHANNEL.
DR PIR: A60959; A60959.
KW Venom; Neurotoxin; Calcium channel inhibitor; Amidation.
FT DISULFID 3 19
FT DISULFID 10 24
FT DISULFID 18 34
FT MOD_RES 35 35 AMIDATION.
SQ SEQUENCE 35 AA; 3825 MW; CBE6462825350D90 CRC64;

Query Match 15.0%; Score 32.5; DB 1; Length 35;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 17 CRPH-QICNVVAIP 29
Db 3 CLPHNRCNALSGP 16

RESULT 7
PPOX_BOVIN STANDARD; PRT; 28 AA.
AC P56602;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO) (FRAGMENTS).
GN PPOX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=95331315; PubMed=7607249;
RA Taketani S., Yoshinaga T., Furukawa T., Kohno H., Tokunaga R.,
RA Nishimura K., Inokuchi H.;
RT "Induction of terminal enzymes for heme biosynthesis during
RT differentiation of mouse erythroleukemia cells.";
RL Eur. J. Biochem. 230:760-765(1995).
CC -1- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRINOGEN
CC IX TO FORM PROTOPORPHYRIN IX.
CC -1- CATALYTIC ACTIVITY: PROTOPORPHYRINOGEN-IX + O(2) -> PROTOPORPHYRIN-
CC IX + H(2)O(2).
CC -1- COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARITY).
CC -1- PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRANE
CC WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
KW Porphyrin biosynthesis; Heme biosynthesis; Oxidoreductase;
KW Flavoprotein; FAD; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 13 14
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2777 MW; FEDFC3F09CB6A345 CRC64;

Query Match 14.4%; Score 31; DB 1; Length 28;

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Best Local Similarity 42.9%; Pred. No. 5e+02; Mismatches 3; Indels 5; Gaps 0;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 25 VVAIPGNASMDAVC 38
    || : | | : | : |
Db 4 VVVLGGGSGDSLC 17

RESULT 8
CYOL_VIOOD
ID CYOL_VIOOD STANDARD; PRT; 30 AA.
AC P82230; 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYCLOVIOOLACIN O1.
OS Viola odorata (Sweet violet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Violaceae; Viola.
OX NCBI_TaxID=97441;
RN [1]
RP SEQUENCE.
RX MEDLINE=20069951; PubMed=10600388;
RA Craik J.D., Daly N.D., Bond T., Waite C.;
RT "Plant cyclotides - a unique family of cyclic and knotted proteins
RT that defines the cyclic cysteine knot structural motif.";
RL J. Mol. Biol. 294:1327-1336(1999).
CC -1- PTM: THIS IS A CYCLIC PEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE CYCLOTIDE FAMILY.
CC -1- CAUTION: THIS PEPTIDE BEING CYCLIC, ITS SEQUENCE WAS ARBITRARILY
CC CHOSEN TO START AT THE POSITION SHOWN BELOW. AS THE DNA SEQUENCE
CC FROM WHICH IT IS DERIVED IS NOT YET KNOWN, IT IS NOT POSSIBLE TO
CC ASSIGN THE CORRECT N- AND C-TERMINI.
FT DISULFID 2 17
FT DISULFID 7 22
FT DISULFID 15 28
SQ SEQUENCE 30 AA; 3141 MW; A3D8CA231098E7E7 CRC64;

Query Match 14.4%; Score 31; DB 1; Length 30;
Best Local Similarity 37.5%; Pred. No. 5.4e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 23 CNVVAIPGNASMDAVC 38
    | | | : | : | : |
Db 7 CTVTALLGSCSNVC 22

RESULT 9
CYLA_PSYLO
ID CYLA_PSYLO STANDARD; PRT; 31 AA.
AC P56872; P82254;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYCLOPSYCHORIDE A (CPT).
OS Psychotria longipes.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Rubiaceae; Psychotria.
OX NCBI_TaxID=41680;
RN [1]
RP SEQUENCE.
RX MEDLINE=95230294; PubMed=7714530;
RA Witherup K.M., Bogusky M.J., Anderson P.S., Ramjit H., Ransom R.W.,
RA Wood T., Sardana M.;
RT "Cyclopsychotride A, a biologically active, 31-residue cyclic peptide
RT isolated from Psychotria longipes.";
RL J. Nat. Prod. 57:1619-1625(1994).
RN [2]
RP SYNTHESIS, AND ANTIBACTERIAL ACTIVITY.
RX MEDLINE=99362685; PubMed=10430870;

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Tam J.P., Lu Y.-A., Yang J.-L., Chiu K.-W.;
"An unusual structural motif of antimicrobial peptides containing
end-to-end macrocycle and cystine-knot disulfides.";
Proc. Natl. Acad. Sci. U.S.A. 96:8913-8918(1999).
-1- FUNCTION: PROBABLY PARTICIPATES IN A PLANT DEFENSE MECHANISM. HAS
ANTIBIOTIC ACTIVITY. INHIBITS NEUTROPHIL BINDING. ACTIVE AGAINST
BOTH GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
-1- PTM: THIS IS A CYCLIC PEPTIDE.
-1- SIMILARITY: BELONGS TO THE CYCLOTIDE FAMILY.
-1- CAUTION: THIS PEPTIDE BEING CYCLIC, ITS SEQUENCE WAS ARBITRARILY
CHOSEN TO START AT THE POSITION SHOWN BELOW. AS THE DNA SEQUENCE
FROM WHICH IT IS DERIVED IS NOT YET KNOWN, IT IS NOT POSSIBLE TO
ASSIGN THE CORRECT N- AND C-TERMINI.
KW Antibiotic.
FT DISULFID 2 17 BY SIMILARITY.
FT DISULFID 7 22 BY SIMILARITY.
FT DISULFID 15 29 BY SIMILARITY.
SQ SEQUENCE 31 AA; 3255 MW; ACC0BBB232ED0CD0 CRC64;

Query Match 13.9%; Score 30; DB 1; Length 31;
Best Local Similarity 37.5%; Pred. No. 7.5e+02;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 23 CNVVAIPGNASMDAVC 38
    | | | : | : |
Db 7 CTVTALLGSCSKVC 22

RESULT 10
BD01_BOVIN
ID BD01_BOVIN STANDARD; PRT; 38 AA.
AC P46159;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA-DEFENSIN 1 (BNBD-1) (BNBD-1).
GN DEFB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX STRAIN=HEREFORD; TISSUE=Neutrophils;
RX MEDLINE=93203264; PubMed=8454635;
RA Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA Smith W., Henschen A.H., Cullor J.S.;
RT "Purification, primary structures, and antibacterial activities of
RT beta-defensins, a new family of antimicrobial peptides from bovine
RT neutrophils.";
RL J. Biol. Chem. 268:6641-6648(1993).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI ML35
    BUT NOT AGAINST S. AUREUS 502A.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC -1- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
CC HSSP; P46170; 1BNB.
DR InterPro; IPR001271; Defensin.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM000048; DEFSN; 1.
KW Antibiotic.
FT DISULFID 5 34 BY SIMILARITY.
FT DISULFID 12 27 BY SIMILARITY.
FT DISULFID 17 35 BY SIMILARITY.
SQ SEQUENCE 38 AA; 4278 MW; 48B872D1025E1A68 CRC64;

Query Match 13.9%; Score 30; DB 1; Length 38;
Best Local Similarity 21.9%; Pred. No. 9.2e+02;
Matches 7; Conservative 8; Mismatches 11; Indels 6; Gaps 1;

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QY 7 FNTSTSDICRPHQICNVVAIPGNASMDAVC 38
   1:  : 111: 11:
Db 2 FASCHNGGICLPNR-----CPGHMIQIGIC 27

RESULT 11
DIDH_PSESP
ID DIDH_PSESP STANDARD; PRT; 15 AA.
AC P80701;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 3-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.50) (3-ALPHA-HSD)
DE (HYDROXYPROSTAGLANDIN DEHYDROGENASE) (HSD29) (FRAGMENT).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE.
RX MEDLINE=97100200; PubMed=8944761;
RA Oppermann U.C.T., Maser E.;
RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl
RL Eur. J. Biochem. 241:744-749(1996).
CC -!- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND
CC A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL
CC COMPOUNDS, INCLUDING A METRAPONE-BASED CLASS OF INSECTICIDES, TO
CC THE RESPECTIVE ALCOHOL METABOLITES.
CC -!- CATALYTIC ACTIVITY: ANDROSTERONE + NAD(P)(+) =
CC 5-ALPHA-ANDROSTANE-3,17-DIONE + NAD(P)H.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC InterPro: IPR002198; ADH_short.
DR PROSITE: PS00061; ADH_SHORT; PARTIAL.
KW Oxidoreductase; NAD.
FT DOMAIN 6 >15 INVOLVED IN COFACTOR BINDING
FT NON_TER 15 15 (BY SIMILARITY).
FT SEQUENCE 15 AA; 1315 MW; 9506860D070A7790 CRC64;

Query Match 13.4%; Score 29; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 25 VVAIPGNAS 33
   1: 111111
Db 2 VIAITGSAS 10

RESULT 12
LEC_CROJU
ID LEC_CROJU STANDARD; PRT; 24 AA.
AC P16352;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LECTIN (FRAGMENT).
OS Crotalaria juncea (Sunn hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Crotalariaeae;
OC Crotalaria.
OX NCBI_TaxID=3829;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Foriers A., de Neve R., Strosberg A.D.;
RT "Lectin sequences as a tool for chemotaxonomical classification.";
RL Physiol. Veg. 17:597-606(1979).
CC -!- SUBUNIT: HOMOTETRAMER.
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CC -!- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
DR PIR; S08293; S08293.
DR HSP; P04122; ILGB.
DR InterPro: IPR000985; Lectin_legA.
DR InterPro: IPR001220; Lectin_legB.
DR Pfam; PF00139; lectin_legB; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; PARTIAL.
DR PROSITE; PS00308; LECTIN_LEGUME_ALPHA; PARTIAL.
KW Lectin; Glycoprotein.
FT NON_TER 24
FT SEQUENCE 24 AA; 2614 MW; 80704D8CD9F9BB6E CRC64;

Query Match 13.4%; Score 29; DB 1; Length 24;
Best Local Similarity 60.0%; Pred. No. 7.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 TFSNTSTSD 15
   1: 111111
Db 5 SFSSTKFTSD 14

RESULT 13
RR2_OCHNE
ID RR2_OCHNE STANDARD; PRT; 34 AA.
AC Q40606;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 (FRAGMENT).
GN RPS2.
OS Ochrosphaera neapolitana.
OC Chloroplast.
OC Eukaryota; Haptophyceae; Isochrysidales; Ochrosphaera.
OX NCBI_TaxID=35137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCMP 593;
RA Huss V.A.R., Tietze A.C., Julius C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X99078; CAA67534.1;
DR InterPro: IPR001865; Ribosomal_S2.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 1
FT SEQUENCE 34 AA; 3640 MW; 2039BA0FB5710655 CRC64;

Query Match 13.4%; Score 29; DB 1; Length 34;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 24 NVVAIPGNASMDAV 37
   1: 111111
Db 1 NLVDIPIPANDDAI 14

RESULT 14
CXAL_CONER
ID CXAL_CONER STANDARD; PRT; 18 AA.
AC P50982;
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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ALPHA-CONOTOXIN EI.
OS Conus ermineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96062516; PubMed=7578057;
RA Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R.,
RA Abramson S.N., McIntosh J.M.;
RT "Alpha-conotoxin EI, a new nicotinic acetylcholine receptor
RT antagonist with novel selectivity.";
RL Biochemistry 34:14519-14526(1995).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; Hydroxylation.
FT DISULFID 4 10
FT DISULFID 5 18
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 2082 MW; 60A61A6C427A6B5E CRC64;

Query Match 13.0%; Score 28; DB 1; Length 18;
Best Local Similarity 45.5%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 15 DICRPHQICNV 25
Db 2 DPCCYHPTCNM 12

RESULT 15
GLUC_PLAFE
ID GLUC_PLAFE STANDARD; PRT; 29 AA.
AC P23062;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE GLUCAGON.
OS Platicthys flesus (European flounder), and
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Platicthys.
OX NCBI_TaxID=8260, 8241,
RN [1]
RP SEQUENCE.
RC SPECIES=P.flesus;
RX MEDLINE=87219793; PubMed=3556313;
RA Conlon J.M., Davis M.S., Thim L.;
RT "Primary structure of insulin and glucagon from the flounder
RT (Platicthys flesus).";
RL Gen. Comp. Endocrinol. 66:203-209(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=T.obesus; TISSUE=Pancreas;
RX MEDLINE=92009094; PubMed=1916209;
RA Navarro I., Gutierrez J., Caixach J., Rivera J., Planas J.;
RT "Isolation and primary structure of glucagon from the endocrine
RT pancreas of Thunnus obesus.";
RL Gen. Comp. Endocrinol. 83:227-232(1991).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

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CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; S09348; GCFLF.
DR PIR; A61135; A61135.
DR HSSP; P01274; IGCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
SQ SEQUENCE 29 AA; 3508 MW; 77D5943208662E52 CRC64;

Query Match 13.0%; Score 28; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GTFSNNTS 12
Db 4 GTFSNDYS 11

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Search completed: February 12, 2002, 12:59:28
Job time: 183 sec

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	121	56.0	30	4	Q9UIH1		Q9uih1 homo sapien
2	41	19.0	36	5	Q9BP43		Q9bp43 conus penna
3	38.5	17.8	37	4	Q9GDB4		Q9gdb4 homo sapien
4	36	16.7	35	12	Q70Z93		Q70z93 human immun
5	36	16.7	35	12	Q70Z94		Q70z94 human immun
6	36	16.7	35	12	Q70Z95		Q70z95 human immun
7	36	16.7	35	12	Q70351		Q70351 human immun
8	35	16.2	26	9	Q9ZXH9		Q9zxh9 bacterioph
9	34.5	16.0	36	6	P79330		P79330 bos taurus
10	34	15.7	33	4	Q9BY50		Q9by50 homo sapien
11	34	15.7	33	12	Q9IEX1		Q9iex1 cotton lea
12	33	15.3	15	11	Q9QUV5		Q9quv5 rattus sp.
13	33	15.3	39	2	Q9PBZ7		Q9pbz7 xytelella fas
14	32	14.8	33	4	Q9UD12		Q9ud12 homo sapien
15	32	14.8	34	12	Q9QLS2		Q9qls2 human aden
16	32	14.8	39	12	Q991P1		Q991p1 human immun
17	32	14.8	39	12	Q991P0		Q991p0 human immun
18	32	14.8	39	12	Q991N9		Q991n9 human immun
19	31.5	14.6	29	6	Q9MZW8		Q9mzw8 pongo pygma

OS Conus pennaceus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF215130; AAG60535.1; -.
FT NON_TER 1
SQ SEQUENCE 36 AA; 3683 MW; 04C74E40FF71141C CRC64;

Query Match 19.0%; Score 41; DB 5; Length 36;
Best Local Similarity 30.8%; Pred. No. 85;
Matches 8; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 3 APGTFSTSTSDICRP----HQICN 24
| | | | | : | | | | : | | : | |
Db 7 ASGKFMVNLKQPLCCPFGGCHLCH 32

RESULT 3
Q9UDB4 PRELIMINARY; PRT; 37 AA.
ID Q9UDB4
AC Q9UDB4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CB8 BETA CHAIN ISOFORM S BETA5 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93170376; PubMed=8436166;
RA Disanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.;
RT "Transcriptional diversity at the duplicated human CD8 beta loci.";
RL Eur. J. Immunol. 23:320-326(1993).
SQ SEQUENCE 37 AA; 3940 MW; 7A4AE1C901E15E99 CRC64;

Query Match 17.8%; Score 38.5; DB 4; Length 37;
Best Local Similarity 34.8%; Pred. No. 2e+02;
Matches 8; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

QY 1 PCAGTFSTSTSDICRPHQIC 23
| | | | | : | | | | : | | : | |
Db 13 PLSPNACMDTMTA----ILQPHRS 32

RESULT 4
Q70293 PRELIMINARY; PRT; 35 AA.
ID Q70293
AC Q70293;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94338597; PubMed=8060542;
RA Bobkov A.F., Garaev M., Rzhabinova A., Kaleebu P., Pitman R.,
RA Weber J.N., Cheingsong-Popov R.;
RT "Molecular epidemiology of HIV-1 in the former Soviet Union: analysis

RT of env V3 sequences and their correlation with epidemiologic data.";
RL AIDS 8:619-624(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93329178; PubMed=8335967;
RA Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,
RA Rzhabinova A., Saukhath S.R., Burdajev N.P., Kolomijets N.D.,
RA Weber J.N.;
RT "Identification of human immunodeficiency virus type 1 subtypes and
RT their distribution in the Commonwealth of Independent States (Former
RT Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
RT analysis.";
RL J. Infect. Dis. 168:292-297(1993).
DR EMBL; U10705; AAA19262.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3852 MW; 5C5827FCBD5DB873 CRC64;

Query Match 16.7%; Score 36; DB 12; Length 35;
Best Local Similarity 47.6%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 2 CAPGTFSTSTST--DICRPH 20
| | | | | : | | | | : | | : | |
Db 14 CAPGQAFYTTGEIGDIRRAH 34

RESULT 5
Q70294 PRELIMINARY; PRT; 35 AA.
ID Q70294
AC Q70294;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94338597; PubMed=8060542;
RA Bobkov A.F., Garaev M., Rzhabinova A., Kaleebu P., Pitman R.,
RA Weber J.N., Cheingsong-Popov R.;
RT "Molecular epidemiology of HIV-1 in the former Soviet Union: analysis
RT of env V3 sequences and their correlation with epidemiologic data.";
RL AIDS 8:619-624(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93329178; PubMed=8335967;
RA Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,
RA Rzhabinova A., Saukhath S.R., Burdajev N.P., Kolomijets N.D.,
RA Weber J.N.;
RT "Identification of human immunodeficiency virus type 1 subtypes and
RT their distribution in the Commonwealth of Independent States (Former
RT Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
RT analysis.";
RL J. Infect. Dis. 168:292-297(1993).
DR EMBL; U10706; AAA19263.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3852 MW; 5C5827FCBD5DB873 CRC64;

Query Match 16.7%; Score 36; DB 12; Length 35;
Best Local Similarity 47.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 2 CAPGTFSTNTSST--DICRPH 20
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Db 14 CAPGQAFYTTGELIGDIRAH 34

RESULT 6

ID Q70295 PRELIMINARY; PRT; 35 AA.

AC Q70295;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94338597; PubMed=8060542;

RA Bobkov A.F., Garaev M., Rzhabinova A., Kaleebu P., Pitman R.,

RA Weber J.N., Cheingsong-Popov R.;

RT "Molecular epidemiology of HIV-1 in the former Soviet Union: analysis

RT of env V3 sequences and their correlation with epidemiologic data.";

RL AIDS 8:619-624(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93329178; PubMed=8335967;

RA Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,

RA Rzhabinova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,

RA Weber J.N.;

RT "Identification of human immunodeficiency virus type 1 subtypes and

RT their distribution in the Commonwealth of Independent States (Former

RT Soviet Union) by serologic V3 peptide-binding assays and V3 sequence

RT analysis.";

RL J. Infect. Dis. 168:292-297(1993).

DR EMBL; U10707; AAA19264.1; -.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

KW Envelope protein.

FT NON_TER 1 1

FT NON_TER 35 35

SQ SEQUENCE 35 AA; 3852 MW; 5C5827FCBD5DB873 CRC64;

Query Match 16.7%; Score 36; DB 12; Length 35;

Best Local Similarity 47.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 2 CAPGTFSTNTSST--DICRPH 20
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Db 14 CAPGQAFYTTGELIGDIRAH 34

RESULT 7

ID Q70351 PRELIMINARY; PRT; 35 AA.

AC Q70351;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94338597; PubMed=8060542;

RA Bobkov A.F., Garaev M., Rzhabinova A., Kaleebu P., Pitman R.,

RA Weber J.N., Cheingsong-Popov R.;

RT "Molecular epidemiology of HIV-1 in the former Soviet Union: analysis

RT of env V3 sequences and their correlation with epidemiologic data.";

RL AIDS 8:619-624(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93329178; PubMed=8335967;

RA Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,

RA Rzhabinova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,

RA Weber J.N.;

RT "Identification of human immunodeficiency virus type 1 subtypes and

RT their distribution in the Commonwealth of Independent States (Former

RT Soviet Union) by serologic V3 peptide-binding assays and V3 sequence

RT analysis.";

RL J. Infect. Dis. 168:292-297(1993).

DR EMBL; U10764; AAA19329.1; -.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

KW Envelope protein.

FT NON_TER 1 1

FT NON_TER 35 35

SQ SEQUENCE 35 AA; 3852 MW; 5C5827FCBD5DB873 CRC64;

Query Match 16.7%; Score 36; DB 12; Length 35;

Best Local Similarity 47.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 2 CAPGTFSTNTSST--DICRPH 20
|||| || || || ||

Db 14 CAPGQAFYTTGELIGDIRAH 34

RESULT 8

Q9ZXKH9 PRELIMINARY; PRT; 26 AA.

ID Q9ZXKH9;

AC Q9ZXKH9;

DT 01-MAY-1999 (TReMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)

DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)

DE PUTATIVE VERTEX HEAD SUBUNIT (FRAGMENT).

GN G24.

OS Bacteriophage ARI.

OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;

OC T4-like phages.

OX NCBI_TaxID=66711;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ARI.

RA Syu W.J., Ding H.C., Seah J.N., Wu K.M., Yu S.L., Tam M.F.,

RA Chang Y.C.;

RT "Characterization of ARI coliphage specific to enterohemorrhagic

RT Escherichia coli O157:H7.";

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF022930; AAD01756.1; -.

FT NON_TER 26 26

SQ SEQUENCE 26 AA; 2830 MW; 5875E0CFBB665934 CRC64;

Query Match 16.2%; Score 35; DB 9; Length 26;

Best Local Similarity 50.0%; Pred. No. 4.3e+02;

Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 8 SNTTSSSTDICRPHQICNVVA 27
|||| || || || ||

Db 11 STTNSNSIGRP----NLVA 26

RESULT 9

P79330 PRELIMINARY; PRT; 36 AA.

ID P79330;

AC P79330;

DT 01-MAY-1997 (TReMBLrel. 03, Created)

DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)

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DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE AGRCAN EPIDERMAL GROWTH FACTOR-LIKE DOMAIN-1 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CARTILAGE PROTEOGLYCAN;
RA MEDLINE=97079270; PubMed=8921002;
RX Fulop C., Cs-Szabo G., Glant T.T.;
RT "Species-specific alternative splicing of the epidermal growth factor-
RT like domain I of cartilage aggrecan.";
RL Biochem. J. 319:935-940(1996).
DR EMBL; L29486; AAB48067.1; -.
FT NON_TER 1
SQ SEQUENCE 36 AA; 3614 MW; 9F6C32F15D3BC9DB CRC64;

Query Match 16.0%; Score 34.5; DB 6; Length 36;
Best Local Similarity 34.8%; Pred. No. 6.9e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 1 PCAPGTFSTSTSDICRPHQIC 23
   ||: || | | |
Db 9 PCSAGTCQETEG-----HWIC 24

RESULT 10
ID Q9BYSO PRELIMINARY; PRT; 33 AA.
AC Q9BYSO;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE KERATIN ASSOCIATED PROTEIN 2.1B (FRAGMENT).
GN KRTAP2.1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SCALP;
RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
RT "Characterization of a cluster of human high/ultrahigh keratin
RT associated proteins on chromosome 17q12-21.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ406929; CAC27568.1; -.
FT NON_TER 1
SQ SEQUENCE 33 AA; 3420 MW; 1DAC91CBB7120302 CRC64;

Query Match 15.7%; Score 34; DB 4; Length 33;
Best Local Similarity 41.2%; Pred. No. 7.5e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PCAPGTFSTSTSDIC 17
   || | | | | |
Db 17 PCGQTPCSTTCRTSSC 33

RESULT 11
ID Q9IEX1 PRELIMINARY; PRT; 33 AA.
AC Q9IEX1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE AC4 PROTEIN (FRAGMENT).
GN AC4.
OS cotton leaf curl virus.

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OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=53010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P12-IR;
RX MEDLINE=20318672; PubMed=10859391;
RA Sanz A.I., Fraile A., Garcia-Arenal F., Zhou X., Robinson D.J.,
RA Khalid S., Butt T., Harrison B.D.;
RT "Multiple infection, recombination and genome relationships among
RT begomovirus isolates found in cotton and other plants in Pakistan.";
RL J. Gen. Virol. 81:1839-1849(2000).
DR EMBL; AJ270854; CAB97069.1; -.
DR InterPro; IPR002488; Geminl_C4.
DR Pfam; PF01492; Geminl_C4; 1.
FT NON_TER 33
SQ SEQUENCE 33 AA; 3478 MW; F3121B92E34ED31E CRC64;

Query Match 15.7%; Score 34; DB 12; Length 33;
Best Local Similarity 41.7%; Pred. No. 7.5e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 NTTSTSDICRPH 20
   | : | : |||
Db 15 NSNAGTTVLRRPH 26

RESULT 12
ID Q9QUY5 PRELIMINARY; PRT; 15 AA.
AC Q9QUY5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE OLIGODENDROCYTE-SPECIFIC UDP-GALACTOSE-CERAMIDE GALACTOSYLTRANSFERASE
DE (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96085162; PubMed=8521863;
RA Schulte S., Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate
RT transporter. Copurification, separation and characterization of the
RT two glycoproteins.";
RL Eur. J. Biochem. 233:947-953(1995).
SQ SEQUENCE 15 AA; 1657 MW; 84474749A06BFFCC CRC64;

Query Match 15.3%; Score 33; DB 11; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PGTFSTNTS 12
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Db 2 PGIFXSTTS 10

RESULT 13
ID Q9PBZ7 PRELIMINARY; PRT; 39 AA.
AC Q9PBZ7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN XF1988.
GN XF1988.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kurame E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.V., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terezi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE004018; AAF84790.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 39 AA; 4501 MW; E085D64BE286D612 CRC64;
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Query Match 15.3%; Score 33; DB 2; Length 39;
Best Local Similarity 37.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 6 TFSNTSSTDICRPHQ 21
Db 24 SLKVTVSADVMRAHR 39

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RESULT 14
Q9UD12 PRELIMINARY; PRT; 33 AA.
AC Q9UD12;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AMGX PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95322983; PubMed=7599636;
RA Lench N.J., Winter G.B.;
RT "Characterisation of molecular defects in X-linked amelogenesis
RT imperfecta (AIH1).";
RL Hum. Mutat. 5:251-259(1995).
SQ SEQUENCE 33 AA; 3681 MW; D131F784BD7D8C93 CRC64;
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Query Match 14.8%; Score 32; DB 4; Length 33;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
Matches 7; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 1 PCAPGTFSTSTSDICRPHQICNVV 26

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Db 8 PCSPCRSHILCRSPCSPCLPCLFI 33
RESULT 15
Q9QL92 PRELIMINARY; PRT; 34 AA.
AC Q9QL92;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 7.7 KDA PROTEIN.
OS Human adenovirus type 7a.
OX Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S-1058;
RA Inada T., Mukoyama A., Yamadera S., Hashido M., Inoue S.;
RT "Epidemiology and genomic analysis of hexon, fiber and E3 region genes
RT of adenovirus type 7 in Japan.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI04382; AAF14124.1; -.
SQ SEQUENCE 34 AA; 3939 MW; DF0B17CA2DA99972 CRC64;
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Query Match 14.8%; Score 32; DB 12; Length 34;
Best Local Similarity 38.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 TTSSTDICRPHQI 22
Db 16 TTLNHDMAKPHYL 28

Search completed: February 12, 2002, 12:59:11
Job time: 181 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:54:04 ; Search time 23.57 Seconds
(without alignments)
122.565 Million cell updates/sec

Title: US-09-800-909-2_COPY_163_201

Perfect score: 216

Sequence: 1 PCAPGTFNSTSTDCRPHQICNVVAIPGNASMDVACT 39

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 262775

Minimum DB seq length: 0

Maximum DB seq length: 39

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

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22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	21.3	17	20	AAW95323
2	46	21.3	38	20	AAW12433
3	42	19.4	36	21	AAW37394
4	41	19.0	17	21	AAW51961
5	41	19.0	17	21	AAW51973
6	40	18.5	28	21	AAW64941
7	39	18.1	25	22	AAW16871
8	39	18.1	25	22	AAW29355
9	39	18.1	25	22	AAW04573
10	39	18.1	26	20	AAW24434
11	37.5	17.4	34	21	AAW44864

12	37	17.1	22	21	AAW51542	Yada homologous pe
13	37	17.1	23	20	AAW73416	Human secreted pro
14	37	17.1	27	22	AAW19434	Peptide #5968 enco
15	37	17.1	27	22	AAW32357	Peptide #6394 enco
16	37	17.1	37	22	AAW19721	Peptide #6155 enco
17	37	17.1	37	22	AAW32991	Peptide #7028 enco
18	36	16.7	22	16	AAW70346	NF-AT transcrip
19	36	16.7	22	21	AAW96558	Human NF-ATc1 anti
20	36	16.7	22	22	AAW66490	Human NF-AT peptid
21	36	16.7	23	19	AAW65481	Hepatitis B surfac
22	36	16.7	23	20	AAW97502	Antigenic site of
23	36	16.7	27	22	AAW80444	Gene #21 associate
24	36	16.7	28	14	AAW37510	I(21Cys, 22-32Pept
25	36	16.7	32	19	AAW65475	Hepatitis B surfac
26	36	16.7	32	19	AAW65476	Hepatitis B surfac
27	36	16.7	32	19	AAW65479	Hepatitis B surfac
28	36	16.7	32	19	AAW65480	Hepatitis B surfac
29	36	16.7	35	22	AAW28490	Peptide #2527 enco
30	36	16.7	38	20	AAW02252	A F-box protein se
31	36	16.7	38	22	AAW19313	Peptide #5747 enco
32	36	16.7	38	22	AAW32087	Peptide #6124 enco
33	35.5	16.4	17	11	AAW06092	Immunoreactive pep
34	35.5	16.4	35	22	AAW35518	Peptide #9555 enco
35	35.5	16.4	37	21	AAW91614	Human secreted pro
36	35	16.2	23	21	AAW27643	Human secreted pro
37	35	16.2	25	19	AAW44915	Spacer peptide for
38	35	16.2	27	17	AAW04374	Mu-conotoxin precu
39	35	16.2	31	6	AAW50156	Sequence of synthe
40	35	16.2	35	19	AAW44920	Spacer peptide for
41	35	16.2	36	18	AAW01811	Human papillomavir
42	35	16.2	39	22	AAW16939	Peptide #3373 enco
43	35	16.2	39	22	AAW29424	Peptide #3461 enco
44	35	16.2	39	22	AAW04632	Peptide #3314 enco
45	34.5	16.0	17	22	AAW05310	R1 and R2 peptide

ALIGNMENTS

RESULT 1

AAW95323

ID AAW95323 standard; Protein; 17 AA.

AC AAW95323;

XX

DT 15-MAR-1999 (first entry)

XX

DE Costant and variable domain sequence of C. psitacci CPS92-106.

XX

KW Chlamydia; cryptic phase; elementary body phase; replicating; probenicid;

KW antiporphyrin acid; immune response; infection; diagnostic; assay; MOMP;

KW major outer membrane protein; autoImmune; inflammatory; porphyria;

KW Ebstein Barr virus; antioxidant.

XX

OS Chlamydia psitacci.

XX

PN WO9500074-A2.

XX

PD 12-NOV-1998.

XX

PF 06-MAY-1998; 98WO-US09237.

XX

PR 18-FEB-1998; 98US-0025521.

PR 06-MAY-1997; 97US-0045689.

PR 06-MAY-1997; 97US-0045739.

PR 06-MAY-1997; 97US-0045779.

PR 06-MAY-1997; 97US-0045780.

PR 06-MAY-1997; 97US-0045784.

PR 06-MAY-1997; 97US-0045787.

PR 14-AUG-1997; 97US-0911593.

PR 18-FEB-1998; 98US-0025174.

PR 18-FEB-1998; 98US-0025176.

XX

PA (UYVA-) UNIV VANDERBILT.
 XX Mitchell WM, Stratton CW;
 PI WPI; 1999-059653/05.
 DR
 XX Composition with two agents effective against different stages of
 PT Chlamydial life cycle - comprises agent targetted against cryptic
 PT phase, against elementary body phase, against replicating phase,
 PT prohenicid and antiporphyric
 XX
 PS Claim 4; Fig 3; 138pp; English.
 XX
 CC The invention relates to the diagnosis and management of infections by
 CC Chlamydia species. The invention provides a composition that comprises
 CC at least two agents, where each of the agents is effective against a
 CC different phase of the chlamydial life cycle. The agents are selected
 CC from: (a) agents targetted against cryptic phase of chlamydial life
 CC cycle; (b) agents targetted against elementary body phase of chlamydial
 CC life cycle; (c) agents targetted against replicating phase of chlamydial
 CC life cycle; (d) prohenicid, and (e) antiporphyric acid. The composition
 CC is used to elicit a protective immune response to Chlamydia infection in
 CC an animal or human and is applied until the animal or human tests
 CC negative for Chlamydia infection. It is also used to treat biological
 CC material infected with Chlamydia. Diagnostic kits for antibody assays
 CC against recombinant major outer membrane protein (MOMP), and for DNA
 CC amplification assays for chlamydial genes, are used to diagnose disease,
 CC e.g. autoimmune disease, an inflammatory disease or a disease that
 CC occurs in an immuno-compromised individual, associated with Chlamydia
 CC infection. The kits are used to detect chlamydial elementary bodies in a
 CC sample. They are also used to monitor and/or modify the course of therapy
 CC in a patient. The treatment reduces the acellular load of infectious
 CC Ebsstein Barr virus. The method is also used to treat porphyria, by
 CC reducing the number of elementary bodies and applying a drug, e.g.
 CC cimetidine, and antioxidants, to reduce the adverse effects associated
 CC with porphyria. Sequences AAW95320 to AAW95323 represent constant and
 CC variable domain sequences of various Chlamydia species.
 XX
 SQ Sequence 17 AA;

Query Match 21.3%; Score 46; DB 20; Length 17;
 Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 CAPGTFSTNTSSD 15
 || || || || || : |
 Db 1 casgtsasnttvaad 14

RESULT 2
 AAY12433
 ID AAY12433 standard; Protein; 38 AA.
 XX
 AC AAY12433;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE Human 5' EST secreted protein SEQ ID NO:464.
 XX
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition.
 OS Homo.sapiens.
 XX
 PN WO9906548-A2.
 XX
 PD 11-FEB-1999.
 PR

PF 31-JUL-1998; 98WO-IB01222.
 XX
 PR 01-AUG-1997; 97US-0905135.
 XX
 PA (GEST) GENSET.
 XX
 XX Duclert A, Dumas Milne Edwards J, Lacroix B;
 PI WPI; 1999-153778/13.
 XX
 DR N-PSDB; AAX41266.
 DR
 XX New nucleic acids encoding human secreted proteins - obtained from
 PT cDNA libraries prepared from e.g. liver, ovary, brain, prostate,
 PT kidney, lung, umbilical cord, placenta and colon tissue
 XX
 PS Claim 27; Page 768-769; 824pp; English.
 XX
 CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12261 to
 CC AAY12514, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.
 XX
 SQ Sequence 38 AA;

Query Match 21.3%; Score 46; DB 20; Length 38;
 Best Local Similarity 40.9%; Pred. No. 30;
 Matches 9; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
 QY 2 CAPGTFSTNTSSDTCRPHQIC 23
 || || || || || : || || ||
 Db 10 crpatldqatratpccrlsggc 31
 RESULT 3
 AAB37394
 ID AAB37394 standard; Peptide; 36 AA.
 XX
 AC AAB37394;
 XX
 DT 20-FEB-2001 (first entry)
 XX
 DE Human secreted peptide #32 encoded by cDNA #47.
 XX

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 OS Homo sapiens.
 XX
 PN WO200058335-A1.
 XX
 PD 05-OCT-2000.
 XX
 XX 22-MAR-2000; 2000WO-US07534.
 XX
 PR 26-MAR-1999; 99US-0126598.
 PR 22-DEC-1999; 99US-0171504.
 PR

CC peroxidases, lysyl oxidases, protein disulfide reductases, tyrosine
 CC oxidases or sulphydryl oxidases is used to formulate compositions
 CC containing active ingredients. (I) is useful for crosslinking protein
 CC layers surrounding active ingredients in food, animal feed and
 CC pharmaceutical products. The compositions can be formulated without
 CC using chemical crosslinking agents. AAY51963-Y51974 represent fragments
 CC of the Pichia pastoris lysyl oxidase protein which is used to
 CC illustrate the method of the invention.

XX
 XX
 SQ Sequence 17 AA;

Query Match 19.0%; Score 41; DB 21; Length 17;
 Best Local Similarity 70.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PCAPGTFSTNT 10
 ||||| ||
 Db 7 pcapgvvynt 16

RESULT 6
 AAY64941
 ID AAY64941 standard; Protein; 28 AA.
 XX
 AC AAY64941;
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Human 5' EST related polypeptide SEQ ID NO:1102.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence;
 KW forensic; location; development; protein synthesis; stability;
 KW regulation; identification.

OS Homo sapiens.
 XX
 PN WO9953051-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 09-APR-1999; 99WO-1B00712.
 XX
 PR 09-APR-1998; 98US-0057719.
 PR 28-APR-1998; 98US-0069047.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-038446/03.
 DR N-PSDB; AA242555.
 XX
 PT Novel secreted protein 5' expressed sequence tag sequences used in
 XX
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures
 XX
 PS Claim 3; Page 687; 837pp; English.

XX
 CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)
 CC sequences, corresponding to human secreted proteins. AAY64651 to
 CC AAY65438 represent the EST-related proteins corresponding to AA242265 to
 CC AA243052. The 5' ESTs can be used for producing secreted human gene
 CC products. They can be used to identify and isolate 5' untranslated
 CC regions (UTRs) and upstream regulatory regions which control the
 CC location, development stage, rate, and quantity of protein synthesis, as
 CC well as stability of mRNA. The ESTs are also useful as probes for
 CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
 CC also be used in forensic procedures to identify individuals, or in
 CC diagnostic procedures to identify individuals having genetic diseases
 CC resulting from abnormal gene expression. The products may also be used in
 CC gene therapy protocols. The nucleic acids encoding signal peptides can be
 CC used for directing extracellular secretion of a polypeptide or the

CC insertion of a polypeptide into a membrane, or importing a polypeptide
 CC into a cell. The proteins encoded by the EST sequences may be useful in
 CC treating a variety of human conditions. Secreted proteins have
 CC therapeutic value, and the identification of new secreted proteins is
 CC valuable. AA242249 to AA242264 and AAY64644 to AAY64650 represent
 CC sequences used in the exemplification of the present invention.

XX
 XX
 SQ Sequence 28 AA;

Query Match 18.5%; Score 40; DB 21; Length 28;
 Best Local Similarity 41.2%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 CAPGTFSTNTSTDICR 18
 | | | | | | | | | |
 Db 10 crpatldqatratpccr 26

RESULT 7
 AAM16871
 ID AAM16871 standard; Protein; 25 AA.
 XX
 AC AAM16871;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Peptide #3305 encoded by probe for measuring cervical gene expression.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US006670.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX
 PT analyzing gene expression in human cervical epithelial cells -
 XX
 PS Claim 27; SEQ ID No 21697; 487pp; English.

XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 XX
 SQ Sequence 25 AA;

Query Match 18.1%; Score 39; DB 22; Length 25;
 Best Local Similarity 45.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PCAPGTFSTNTSSTDCIRPH 20
 | | | | | | | | | |
 Db 3 pwfeglpshsttttsimrrh 22

RESULT 8

AAM29355
 ID AAM29355 standard; Protein; 25 AA.

AC AAM29355;

DT 17-OCT-2001 (first entry)

DE Peptide #3392 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.

XX Homo sapiens.

OS WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00663.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human placenta -

XX Claim 27; SEQ ID No 29624; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs;
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.

XX Sequence 25 AA;

Query Match 18.1%; Score 39; DB 22; Length 25;
 Best Local Similarity 45.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PCAPGTFSTNTSSTDCIRPH 20
 | | | | | | | | | |
 Db 3 pwfeglpshsttttsimrrh 22

RESULT 9

AAM04573
 ID AAM04573 standard; Protein; 25 AA.

XX

AC AAM04573;

DT 09-OCT-2001 (first entry)

DE Peptide #3255 encoded by probe for measuring breast gene expression.

XX Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX Homo sapiens.

XX WO200157270-A2.

XX 09-AUG-2001.

XX 29-JAN-2001; 2001WO-US00661.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX Novel single exon nucleic acid probe used to measuring gene expression

XX in a human breast -

XX Claim 27; SEQ ID No 13313; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes
 CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative
 CC breast disease and non-carcinoma tumours.

XX Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 25 AA;

Query Match 18.1%; Score 39; DB 22; Length 25;
 Best Local Similarity 45.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PCAPGTFSTNTSSTDCIRPH 20
 | | | | | | | | | |
 Db 3 pwfeglpshsttttsimrrh 22

RESULT 10

AAY24434
 ID AAY24434 standard; peptide; 26 AA.

XX AAY24434;

XX 27-SEP-1999 (first entry)

XX Adenovirus hexon protein heterologous ligand #2.
 XX Adenovirus; RGD sequence; adenoviral vector; capsid protein; ligand;

KW infection.
 XX Mastadenovirus.
 OS Synthetic.
 OS
 PN WO9936545-A2.
 XX
 XX 22-JUL-1999.
 PD
 PF 15-JAN-1999; 99WO-US00913.
 XX
 XX 16-JAN-1998; 98US-0071674.
 PR
 XX (GENZ) GENZYME CORP.
 PA
 XX Armentano D, O'Riordan CR, Romanczuk H;
 PI
 XX WPI; 1999-444401/37.
 DR
 XX Adenoviral vectors with modified capsid proteins for improved
 PT infectious capabilities
 PT
 XX Example 1; Fig 1A; 59pp; English.
 PS
 XX The present invention describes an adenoviral capsid protein comprising
 CC a heterologous ligand, where the ligand facilitates binding of the
 CC adenovirus to a target cell. The adenoviral vector is used to transfer a
 CC transgene to a target cell. The heterologous ligand in the adenoviral
 CC capsid protein (especially a fibre or hexon protein or protein IX)
 CC facilitates binding of the vector to the target cell. In particular, the
 CC adenoviral vector can be used to transfer the human cystic fibrosis
 CC transmembrane conductance regulator protein gene to the respiratory
 CC epithelium of test animals. The modified adenoviral capsid proteins
 CC improve and/or alter the infectious capability of the vector. The
 CC present sequence represents an adenovirus hexon protein heterologous
 CC ligand used in an example from the present invention.
 XX
 XX Sequence 26 AA;
 SQ
 Query Match 18.1%; Score 39; DB 20; Length 26;
 Best Local Similarity 47.4%; Pred. No. 1.7e+02;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 8 SNTTSTDCRPHQICNVV 26
 Db 1 snttssdqiasysprv 19
 |||||; |: ||
 1 snttssdqiasysprv 19
 RESULT 11
 AAB44864
 ID AAB44864 standard; Protein; 34 AA.
 XX
 AC AAB44864;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 35.
 XX
 KW Human; secreted protein; cytostatic; antiarthritic; antiasthmatic;
 KW immunosuppressive; antiarteriosclerotic; antiinflammatory; nootropic;
 KW neuroprotective; antidiabetic; tranquiliser; vulnerary; antibacterial;
 KW antipsoriatic; antiarrhythmic; antirheumatic; cardiant; anti-HIV;
 KW autoimmune disorder; allergic condition; cardiovascular disorder;
 KW cancer; neurological disease; tissue repair.
 XX
 OS Homo sapiens.
 XX
 XX WO2000055176-A2.
 PN
 XX 21-SEP-2000.
 PD
 XX 09-MAR-2000; 2000WO-US06057.
 PF

XX
 PR 12-MAR-1999; 99US-0124142.
 PR 11-JUN-1999; 99US-0138597.
 PR 03-DEC-1999; 99US-0168666.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM, Komatsoulis G;
 PI
 XX WPI; 2000-638176/61.
 DR N-PSDB; AAC79883.
 DR
 XX Novel 49 human secreted proteins useful for diagnosis, prevention and
 PT treatment of disorders including neurological, cell proliferative,
 PT cardiovascular, and autoimmune/inflammatory disorders and microbial
 PT infections
 XX
 PS Claim 11; Page 373-374; 405pp; English.
 XX
 XX This invention describes a novel isolated polypeptide (I) comprising an
 CC amino acid sequence at least 95 % identical to a polypeptide sequence
 CC selected from 49 polypeptides encoded by polynucleotide sequences
 CC included in American Type Culture Collection (ATCC) deposit number
 CC 203917, defined in the specification. The products of the invention have
 CC cytostatic, antiarthritic, antiasthmatic, immunosuppressive, nootropic,
 CC antiarteriosclerotic, antiinflammatory, neuroprotective, antidiabetic,
 CC tranquiliser, vulnerary, antibacterial, antipsoriatic, antiarrhythmic,
 CC antirheumatic, cardiant and anti-HIV activity. (I) or a nucleic acid (II)
 CC encoding (I) is useful for preventing, treating or ameliorating a medical
 CC condition and for diagnosing a pathological condition or susceptibility
 CC to the condition. (I) is useful for identifying a binding partner which
 CC affects the activity of the polypeptide and for identifying an activity
 CC in a biological sample. (I), (II) or an antibody (IV) specific to (I) is
 CC also useful for treating or preventing a disease, disorder or condition
 CC associated with aberrant expression of (I). Diseases treated or diagnosed
 CC include immune disorders such as autoimmune diseases, blood protein
 CC disorders, anemia, allergic reactions and conditions such as asthma,
 CC organ rejection or graft-versus-host disease, inflammation, hyper
 CC proliferative disorders, cardiovascular disorders such as arterioarterial
 CC fistula, arrhythmias, arteriosclerosis, coronary thrombosis, organ
 CC regeneration, cancer, neovascular glaucoma, diabetic retinopathy,
 CC rheumatoid arthritis, psoriasis, diseases associated with increased
 CC apoptosis that include acquired immunodeficiency syndrome (AIDS),
 CC neurological diseases such as Parkinson's disease, viral, bacterial,
 CC fungal or parasitic diseases. They are also used to repair, replace or
 CC protect tissue damage by congenital defects, to treat trauma, in surgery,
 CC including cosmetic plastic surgery, to treat fibrosis, reperfusion injury
 CC or systemic cytokine damage, to stimulate chondrocyte growth, to prevent
 CC skin aging due to sunburn, to change a mammal's mental state or physical
 CC state by influencing biorhythms, cardiac rhythms, depression, memory,
 CC stress and for accelerating wound healing. (I), (II) and/or their agonist
 CC or antagonist are useful as food additives or preservatives to increase
 CC or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamin, mineral or other nutritional components. (I) is
 CC useful for screening therapeutic compounds. (II) is useful in forensic
 CC biology for detecting DNA sequences and as diagnostic probes for
 CC detecting the presence of specific mRNA in a particular cell type.
 XX
 XX Sequence 34 AA;
 SQ
 Query Match 17.4%; Score 37.5; DB 21; Length 34;
 Best Local Similarity 33.3%; Pred. No. 3.6e+02;
 Matches 6; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
 QY 6 TFSNTTSTDCRPHQIC 23
 | |::: |: |||
 Db 13 tilniattstlick-hqvc 29
 RESULT 12
 AAB51542
 ID AAB51542 standard; Peptide; 22 AA.

```

XX AC AAB51542;
XX DT 15-FEB-2001 (first entry)
XX DE Yada homologous peptide #5.
XX KW proteobacteria; extracellular domain; virulence determinant; Yada;
XX KW adhesin; proteobacterial infection prevention; vaccine.
XX OS Thiobacillus ferrooxidans.
XX PN WO200061165-A1.
XX PD 19-OCT-2000.
XX PF 13-APR-2000; 2000WO-US09866.
XX PR 13-APR-1999; 99US-0129073.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Lupas AN;
XX DR WPI: 2000-647397/62.
XX PT An isolated polypeptide conserved in proteobacterial extracellular
XX PT domains used in the treatment and prevention of bacterial infections -
XX PS Example 5; Page 59; 85pp; English.
XX CC This invention relates to peptides AAB51512 - AAB51537 which represent
XX CC conserved proteobacterial extracellular domains. Sequences
XX CC AAB51538 - AAB51618 represent peptides homologous to Yada, a Yersinia
XX CC adhesin which is an important virulence determinant of the Yersinia
XX CC species. The invention includes an antibody which binds to the
XX CC proteobacterial extracellular peptides, and an immunogenic composition
XX CC containing the antibody used as a vaccine to prevent infection by a
XX CC proteobacteria. The polypeptides and antibodies are useful in the
XX CC treatment and prevention of proteobacterial infections. The polypeptides
XX CC can also be used to identify compounds which antagonize the binding of a
XX CC bacterial adhesin to its ligand. The host cell can be used to produce
XX CC the polypeptides in a suitable culture system. The composition can be
XX CC used to vaccinate a patient against a proteobacterial infection.
XX SQ Sequence 22 AA;

Query Match 17.1%; Score 37; DB 21; Length 22;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 10; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 3 APGTFSTNTSSDTCRPHQI 22
Db 5 apgtltsqt--stdavngsq 22
      ||||| |||||
      1;

RESULT 13
AAW73416
ID AAW73416 standard; Protein; 23 AA.
XX AC AAW73416;
XX DT 19-FEB-1999 (first entry)
XX DE Human secreted protein encoded by Gene No. 20.
XX KW Secreted protein; human; protein therapy; gene therapy; blood disorder;
XX KW pathological condition; diagnosis; cancer; neurological disorder;
XX KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
XX KW immune system disorder; Alzheimer's disease; cognitive disorder;
XX KW schizophrenia; prostate disease; autoimmune disorder; AIDS.

```

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 23 /note= "unspecified amino acid"
XX PN WO9854206-A1.
XX PD 03-DEC-1998.
XX PF 28-MAY-1998; 98WO-US10868.
XX PR 29-AUG-1997; 97US-0056296.
XX PR 30-MAY-1997; 97US-0044039.
XX PR 30-MAY-1997; 97US-0048093.
XX PR 30-MAY-1997; 97US-0048101.
XX PR 30-MAY-1997; 97US-0048190.
XX PR 30-MAY-1997; 97US-0048356.
XX PR 30-MAY-1997; 97US-0050935.
XX PR 29-AUG-1997; 97US-0056250.
XX PR 29-AUG-1997; 97US-0056293.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Carter KC, Dillon PJ, Endress GA, Feng P, NI J;
XX PI Rosen CA, Ruben SM, Yu G;
XX DR WPI: 1999-070209/06.
XX DR N-PSDB; AAV08830.
XX PT New isolated human genes - useful for diagnosis and treatment of,
XX PT e.g. cancers, neurological disorders, immune diseases, developmental
XX PS disorders or blood disorders
XX PS Claim 11; Page 157; 188pp; English.
XX CC This sequence is encoded by a cDNA of the invention, designated
XX CC Gene No. 20. This sequence represents a human secreted protein, and is
XX CC expressed ubiquitously, including T-cells and amygdala.
XX CC The DNA sequences of the invention and their corresponding secreted
XX CC polypeptides are useful for preventing, treating or ameliorating medical
XX CC conditions, e.g. by protein or gene therapy. Also pathological conditions
XX CC can be diagnosed by determining the amount of the new polypeptides in a
XX CC sample or by determining the presence of mutations in the DNA sequences.
XX CC Specific uses are described for each of the DNA sequences and the encoded
XX CC proteins, based on which tissues they are most highly expressed in, and
XX CC include developing products for the diagnosis or treatment of cancer,
XX CC tumours, neurological disorders, developmental abnormalities and foetal
XX CC deficiencies, blood disorders, leukaemias, diseases of the immune system
XX CC (including allergies or asthma), hepatic disease, Alzheimer's and
XX CC cognitive disorders, schizophrenia, prostate diseases, autoimmune
XX CC disorders and AIDS. The polypeptides are also useful for identifying
XX CC their binding partners.
XX SQ Sequence 23 AA;

Query Match 17.1%; Score 37; DB 20; Length 23;
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 CAPGTFSTNTSSDTC 17
Db 5 cgpagaagtacssac 20
      ||| |||
      1;

RESULT 14
AAM19434
ID AAM19434 standard; Protein; 27 AA.
XX AC AAM19434;
XX XX

```

DT 12-OCT-2001 (first entry)
XX Peptide #5868 encoded by probe for measuring cervical gene expression.
DE Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX Homo sapiens.
OS
XX WO200157278-A2.
PN 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US006670.
PF 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
PI Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
PT Claim 27; SEQ ID No 24260; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 27 AA;

Query Match 17.1%; Score 37; DB 22; Length 27;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 19 PHQICN 24
Db 13 phqlcn 18

RESULT 15
AAM32357
ID AAM32357 standard; Protein; 27 AA.
XX
AC AAM32357;
XX
DT 17-OCT-2001 (first entry)
XX Peptide #6394 encoded by probe for measuring placental gene expression.
DE Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX Homo sapiens.
OS

PN WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US006663.
PF 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
PI Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
PT Claim 27; SEQ ID No 32626; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENPs:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 27 AA;

Query Match 17.1%; Score 37; DB 22; Length 27;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 19 PHQICN 24
Db 13 phqlcn 18

Search completed: February 12, 2002, 12:56:04
Job time: 120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:54:29 ; Search time 12.56 Seconds
(without alignments)
69.875 Million cell updates/sec

Title: US-09-800-909-2_COPY 163_201

Perfect score: 216
Sequence: 1 PCAPGTFSTTSSDTCRPHQICNVVAIPGNASMDAVCT 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 144239

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Minimum DB seq length: 0
Maximum DB seq length: 39
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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Database : Issued_Patents_Aa:*
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3: /cgn2_6/pdata2/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata2/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata2/1aa/PTCTUS_COMB.pep:*
6: /cgn2_6/pdata2/1aa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	216	100.0	39	1	US-08-050-319B-41	Sequence 41, Appl
2	216	100.0	39	2	US-08-465-982-41	Sequence 41, Appl
3	77	35.6	15	6	5395760-10	Patent No. 5395760
4	72	33.3	15	1	US-08-221-583-45	Sequence 45, Appl
5	72	33.3	15	1	US-08-221-583-46	Sequence 46, Appl
6	72	33.3	15	5	PCT-US95-04018-45	Sequence 45, Appl
7	72	33.3	15	5	PCT-US95-04018-46	Sequence 46, Appl
8	71	32.9	15	1	US-08-221-583-44	Sequence 44, Appl
9	71	32.9	15	5	PCT-US95-04018-44	Sequence 44, Appl
10	70	32.4	15	1	US-08-221-583-49	Sequence 49, Appl
11	70	32.4	15	5	PCT-US95-04018-49	Sequence 49, Appl
12	67	31.0	15	1	US-08-221-583-47	Sequence 47, Appl
13	67	31.0	15	5	PCT-US95-04018-47	Sequence 47, Appl
14	66	30.6	15	1	US-08-221-583-48	Sequence 48, Appl
15	66	30.6	15	5	PCT-US95-04018-48	Sequence 48, Appl
16	57	26.4	15	1	US-08-221-583-50	Sequence 50, Appl
17	57	26.4	15	5	PCT-US95-04018-50	Sequence 50, Appl
18	48	22.2	20	2	US-08-126-016-24	Sequence 24, Appl
19	45	20.8	15	1	US-08-221-583-51	Sequence 51, Appl
20	45	20.8	15	5	PCT-US95-04018-51	Sequence 51, Appl
21	39	18.1	23	3	US-09-101-146-58	Sequence 58, Appl
22	37.5	17.4	20	2	US-08-126-016-25	Sequence 25, Appl
23	36	16.7	22	2	US-08-124-981A-28	Sequence 28, Appl
24	36	16.7	22	3	US-09-037-190-31	Sequence 31, Appl
25	36	16.7	22	3	US-09-037-192-31	Sequence 31, Appl
26	36	16.7	22	3	US-09-037-143-31	Sequence 31, Appl
27	36	16.7	22	4	US-09-049-691-31	Sequence 31, Appl

ALIGNMENTS

```

1
RESULT
US-08-050-319B-41
; Sequence 41, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
IS-08-050-319B-41

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Query Match 100.0%; Score 216; DB 1; Length 39;

Query Match 100.0%; Score 216; DB 1;

Best Local Similarity 100.0%; Pred. No. 3.9e-22;
Matches 39; Conservative 0; Mismatches 0; Indels

QY 1 PCAPGTFSTTSS"DICRPHQICNVVAIPGNASMDAVCT 39

db 1 PCAPGTFSTTSSTDCRPHOICNVVATPGNASMDAVCT 39

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;; STREET: One Liberty Place 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19403
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25:mdctcMod.
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/221,583
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: CCOR-0185
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-221-583-46

Query Match 33.3%; Score 72; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 SNTSSTDICRPHQI 22
Db 1 SNTSSTDICRPHQI 15

RESULT 6
PCT-US95-04018-45
;; Sequence 45, Application PC/TUS9504018
;; GENERAL INFORMATION:
;; APPLICANT: Heavner, George A.
;; APPLICANT: Kruszynski, Marian
;; APPLICANT: Mervic, Miljenko
;; APPLICANT: Weber, Robert W.
;; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
;; NUMBER OF SEQUENCES: 76
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: Norris
;; STREET: One Liberty Place 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19403
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04018
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/221,580
;; FILING DATE: 01-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/221,583

;; FILING DATE: 01-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/221,581
;; FILING DATE: 01-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: CCOR-0232
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US95-04018-45

Query Match 33.3%; Score 72; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTFSTSTSTDIARP 19
Db 1 GTFSTSTSTDIARP 15

RESULT 7
PCT-US95-04018-46
;; Sequence 46, Application PC/TUS9504018
;; GENERAL INFORMATION:
;; APPLICANT: Heavner, George A.
;; APPLICANT: Kruszynski, Marian
;; APPLICANT: Mervic, Miljenko
;; APPLICANT: Weber, Robert W.
;; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
;; NUMBER OF SEQUENCES: 76
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: Norris
;; STREET: One Liberty Place 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19403
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04018
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/221,580
;; FILING DATE: 01-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/221,583
;; FILING DATE: 01-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/221,581
;; FILING DATE: 01-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: CCOR-0232
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-46

Query Match 33.3%; Score 72; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SNTTSSTDICRPHQI 22
| | | | | | | | | | | | | | | |
Db 1 SNTTSSTDICRPHQI 15

RESULT 8
US-08-221-583-44
; Sequence 44, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25;mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-44

Query Match 32.9%; Score 71; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APGTFSTNTSSTDI 16
| | | | | | | | | | | | | | | |
Db 2 APGTFSTNTSSTDI 15

RESULT 9
PCT-US95-04018-44
; Sequence 44, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko

APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-44

Query Match 32.9%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APGTFSTNTSSTDI 16
| | | | | | | | | | | | | | | |
Db 2 APGTFSTNTSSTDI 15

RESULT 10
US-08-221-583-49
; Sequence 49, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
; CURRENT/APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-49

Query Match 32.4%; Score 70; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 18 RPHQICNVVAIPGN 31
||||| |||||||
Db 2 RPHQIANVVAIPGN 15

RESULT 11

PCT-US95-04018-49
; Sequence 49, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

;
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-49

Query Match 32.4%; Score 70; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 18 RPHQICNVVAIPGN 31
||||| |||||||
Db 2 RPHQIANVVAIPGN 15

RESULT 12

US-08-221-583-47
; Sequence 47, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-47

Query Match 31.0%; Score 67; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0062;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 11 TSSTDICRPHQICNV 25
||||| |||||||
Db 1 TSSTDIAIRPHQIANV 15

RESULT 13

PCT-US95-04018-47
; Sequence 47, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian

; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-47

Query Match 31.0%; Score 67; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0062;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 TSSTDICRPHQICNV 25
| | | | | | | | | |
DB 1 TSSTDICRPHQIANV 15

RESULT 14
US-08-221-583-48
; Sequence 48, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25.mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-221-583-48

Query Match 30.6%; Score 66; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0084;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 TDIARPHQICNVVAVI 28
| | | | | | | | | |
DB 1 TDIARPHQIANVAVI 15

RESULT 15
PCT-US95-04018-48
; Sequence 48, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-48

Query Match 30.6%; Score 66; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0084;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 TDICRPHQICNVVAI 28
 | | | | | | | | | |
Db 1 TDIARPHQIANVVAI 15

Search completed: February 12, 2002, 12:56:23
Job time: 114 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 12:58:45 ; Search time 13.29 Seconds
(without alignments)
326.708 Million cell updates/sec

Title: . US-09-800-909-2_COPY_201_257

Perfect score: 302
Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSELLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 13308

```
Minimum DB seq length: 0
Maximum DB seq length: 57
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :      PIR_68:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	71	23.5	54	2	A60726	mucin, gallbladder
2	56.5	18.7	52	2	S63324	hypothetical prote
3	55.5	18.4	42	2	I70082	glycoprotein Ib al
4	51	16.9	25	2	I40692	cenA protein (IgaI
5	50	16.6	46	2	S07073	arabinogalactan pr
6	47	15.6	31	2	T36022	small hypothetical
7	44.5	14.7	57	2	S10782	salivary protein p
8	44.5	14.7	57	2	S15587	hypothetical prote
9	43.5	14.6	28	2	S6139	MHC class I HLA-J
10	43.5	14.4	47	2	S32108	sepiapterin reduct
11	43.5	14.4	54	2	D81737	hypothetical prote
12	43	14.2	31	2	I54515	pre-B cell Ig lamb
13	43	14.2	39	2	A46662	collagen alpha 2(V
14	42	13.9	36	2	A31712	collagen alpha 1(X
15	42	13.9	48	2	I46522	troponin T 2fa - r
16	42	13.9	55	2	S08424	H+-transporting AT
17	42	13.9	55	2	T11184	H+-transporting AT
18	41	13.6	42	2	T07030	extensin - tomato
19	40.5	13.4	50	2	A29789	mucin - sheep (fra
20	40	13.2	29	2	G39690	neural cell adhesi
21	40	13.2	50	2	H64801	hypothetical prote
22	40	13.2	50	2	A33756	dorsal protein - f
23	40	13.2	51	2	G72801	gp18 protein - Myc
24	40	13.2	52	2	S58216	hypothetical prote
25	40	13.2	54	2	T11131	ATP synthase subun
26	40	13.2	55	2	T11105	H+-transporting AT
27	40	13.2	57	2	I58120	gene insl protein
28	39.5	13.1	52	2	S01945	myosin catalytic 1
29	39	12.9	27	2	S51176	aspartate transcar

30	39	12.9	53	2	S17672	hypothetical prote
31	38.5	12.7	51	2	C8117	hypothetical prote
32	38	12.6	53	2	S23202	kappa-casein - bov
33	38	12.6	54	2	S14338	serpin I - horse (
34	38	12.6	55	2	S29770	DNA-binding protei
35	38	12.6	55	2	A37238	autoimmune epitope
36	37.5	12.4	49	2	S25433	neural cell adhesi
37	37.5	12.4	51	2	T29481	hypothetical prote
38	37.5	12.4	57	2	E41715	hypothetical prote
39	37.5	12.4	57	2	T36648	hypothetical prote
40	37	12.3	30	2	JC1360	hypothetical 3K pr
41	37	12.3	38	2	S68260	hypothetical prote
42	37	12.3	45	2	S24713	Ig alpha chain, tr
43	37	12.3	49	2	S72213	beta-fructofuranos
44	37	12.3	51	2	B32040	dihydrolipoamide S
45	37	12.3	55	2	A82795	hypothetical prote

ALIGNMENTS

```

RESULT      1
             mucin, gallbladder - bovine (fragments)
             A60726
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C:Accession: A60726
R:Afdhal, N.H.; Offner, G.D.; Smith, B.F.
Gastroenterology 99, 1493-1501, 1990
A:Title: Characterization of bovine gallbladder mucin. Amino acid sequences
A:Reference number: A60726; MUID:910007106
A:Accession: A60726
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-54 <AFD>

```

Query Match 23.5%; Score 71; DB 2; Length 54;
 Best Local Similarity 35.2%; Pred. NO. 2.3;
 Matches 19: Conservative 6; Mismatches 25; Indels 4; Gaps 2;

```
QY      2 STSTRSMAPCAVHLQPVPVSTRSQHT-QPTPESTAPSTSF---LLPMGPSPPA 51
       :|::: ||: | |: | | | | | | | | | | | | | | | | | | | |
Dh      1 TTTTPNVTPIPGSGPOTMPTSSPIPETPTMTSTPPTVGGPSSPDTEPSGPPPS 54
```

RESULT 2

S63324 hypothetical protein YNL338w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein N0170
C:Species: *Saccharomyces cerevisiae*
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 05-Nov-1999
C:Accession: S63324
R:Obermaier, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63317
A:Accession: S63324
A:Molecule type: DNA
A:Residues: 1-52 <OBE>
A:Cross-references: EMBL:271614; NID:gl302466; PID:e239576; PID:gl302467; G
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YNL338w
A:Map position: 14L

Query Match	18.7%	Score 56.5;	DB 2;	Length 52;
Best Local Similarity	35.7%;	Pred. No.	42;	
Matches 15;	Conservative	4;	Mismatches	20; Indels
				3; Gaps
Qy	8	SMAGVAVHLPQVTRSQHTQTPEPSTAPSTFLLPMGPSP	49	
		:::		: :
Db	11	SMQSDVIYPTETTHTHT--PTPHH--PTHHTHTHHNP	49	

A;Residues: 1-52 <OBE>
A:Cross-references: EMBL:271614: NID:q1302466: PID:e239576: PID:q1302467: GSPDB:GN000

RESULT 3

I70082
glycoprotein Ib alpha variant B - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I70082
R:Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t
ations.
A:Reference number: I53355; MUID:92250564
A:Accession: I70082
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: GB:S34439; NID:g249178; PID:AAB22153.1; PID:g249179
C:Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r
C:Keywords: glycoprotein

Query Match 18.4%; Score 55.5; DB 2; Length 42;

Best Local Similarity 35.6%; Pred. No. 41;

Matches 16; Conservative 6; Mismatches 18; Indels 5; Gaps 3;

QY 5 PTRSMAPGAVHLPQVSTRSQHTPTPEPTAPSTFLLPMGPSP 49

Db 2 PTSEPAAPSPT-TPEPTSEPA-SPTTPEPTSEPA-----PTTPEP 41

RESULT 4

I40692
cena protein (Igalh) - Cellulomonas fimi (fragment)
C:Species: Cellulomonas fimi
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C:Accession: I40692
R:Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren
FEMS Microbiol. Lett. 92, 199-204, 1992
A:Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human Iga
hosaee.
A:Reference number: I40692
A:Accession: I40692
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-25 <RES>
A:Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036

Query Match 16.9%; Score 51; DB 2; Length 25;

Best Local Similarity 46.2%; Pred. No. 60;

Matches 12; Conservative 1; Mismatches 5; Indels 8; Gaps 1;

QY 24 SQHTQPTPEPTAPSTFLLPMGPSP 49

Db 2 SVSTPTPTPTPTPT-----PSP 19

RESULT 5

S07073
arabinogalactan protein - Italian ryegrass (fragments)
C:Species: Lolium multiflorum (Italian ryegrass)
C:Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998
C:Accession: S07073
R:Gleeson, P.A.; McNamara, M.; Wattenhall, R.E.H.; Stone, B.A.; Fincher, G.B.
Biochem. J. 264, 857-862, 1989
A:Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-
A:Reference number: S07073; MUID:90147544
A:Accession: S07073
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <GLE>
A:Note: 19-His and 23-Leu were also found

C:Keywords: hydroxyproline
F:6,7,9,11,14,16,18,20,26,30,34,36,39/Modified site: hydroxyproline (Pro) #status exp

Query Match 16.6%; Score 50; DB 2; Length 46;

Best Local Similarity 37.1%; Pred. No. 1.4e+02;

Matches 13; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 17 PQPVSTRSQHTPTPEPTAPSTFLLPMGPSPPA 51

Db 6 PPAPAKAPAPVPEASTAPVAA--PTTXPSPPA 38

RESULT 6

T36022
small hypothetical protein SCC54.09c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36022
R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21581
A:Accession: T36022
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-31 <SEE>
A:Cross-references: EMBL:AL035591; PIDN:CAB38139.1; GSPDB:GN00070; SCOEDB:SCC54.09c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCC54.09c

Query Match 15.6%; Score 47; DB 2; Length 31;

Best Local Similarity 30.4%; Pred. No. 1.7e+02;

Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 19 PVSTRSQHTPTPEPTAPSTSF 41

Db 2 PLAARNEDNEPVPAPTWTGTGF 24

RESULT 7

S10782
salivary protein P-B - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10782
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A:Reference number: S10780; MUID:90336641
A:Accession: S10782
A:Molecule type: protein
A:Residues: 1-57 <STR>
C:Superfamily: proline-rich peptide P-B

Query Match 14.7%; Score 44.5; DB 2; Length 57;

Best Local Similarity 28.8%; Pred. No. 5.3e+02;

Matches 15; Conservative 2; Mismatches 28; Indels 7; Gaps 2;

QY 5 PTRSMAPGAVHLPQVSTRSQHTPTPEPTAPSTFLLPMGPSPPAESTG 56

Db 4 PRGPVPPGFLAPPQPGF--PGFVPPPPPPYGPGR-----IPPPPPAPYGP 48

RESULT 8

SI6587
hypothetical protein 1 - lamb's-quarters
C:Species: Chenopodium album (lamb's-quarters)
C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: SI6587
R:Doerfel, P.; Weihe, A.; Dolferus, R.; Boerner, T.

```

Plant Mol., Biol. 17, 155-156, 1991
A>Title: DNA sequence of a mitochondrial plasmid from Chenopodium album.
A:Reference number: S16587; MUID:91329724.
A:Accession: S16587
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-57 <DOE>
A:Cross-references: EMBL:X58911

Query Match          14.7%; Score 44.5; DB 2; Length 57;
Best Local Similarity 34.2%; Pred. No. 5.3e+02;
Matches 13; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

Qy 16 LPQPVTRSQHTQTPPEFSTAPSTSFLLPMGSPSPAEG 53
   || : : : | : || : : : | : | : |
Db 21 LPWLRLTLTFRVP-PDPSQAPNHNLSLNPPSAAVG 57

RESULT 9
I56139
MHC class I HLA-J antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56139; I72807

```

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <TET>
A;Cross-references: GB:AE002280; GB:AE002160; NID:g7190162; PIDN:AAF39005.1; PID:g719
A;Experimental source: strain Nigg (MOPn)
C;Genetics:
A;Gene: TC0127

      Query Match      14.4%; Score 43.5; DB 2; Length 54;
      Best Local Similarity 42.9%; Pred. No. 6.1e+02;
      Matches 12; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY      28 QPTPEPSTAPSTSFLLPMGPSPPPAEGST 55
      ||: :|| :|| :|| :|| :|| :|| :||
Db       4 QPSKPSQASSLS-LKGGDPAPPSPGRAT 30

RESULT      12
154515
pre-B cell Ig lambda-like omega light chain (non-rearranging) IGLL2 - human (fragment
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999
C;Accession: I54515

```

Immunogenetics 38, 387-399, 1993
 A:Title: Physical location of the human immunoglobulin lambda-like genes, 14.L, 16.L, 17.L, 18.L, 19.L, 20.L, 21.L, 22.L, 23.L, 24.L, 25.L, 26.L, 27.L, 28.L, 29.L, 30.L, 31.L, 32.L, 33.L, 34.L, 35.L, 36.L, 37.L, 38.L, 39.L, 40.L, 41.L, 42.L, 43.L, 44.L, 45.L, 46.L, 47.L, 48.L, 49.L, 50.L, 51.L, 52.L, 53.L, 54.L, 55.L, 56.L, 57.L, 58.L, 59.L, 60.L, 61.L, 62.L, 63.L, 64.L, 65.L, 66.L, 67.L, 68.L, 69.L, 70.L, 71.L, 72.L, 73.L, 74.L, 75.L, 76.L, 77.L, 78.L, 79.L, 80.L, 81.L, 82.L, 83.L, 84.L, 85.L, 86.L, 87.L, 88.L, 89.L, 90.L, 91.L, 92.L, 93.L, 94.L, 95.L, 96.L, 97.L, 98.L, 99.L, 100.L
 A:Reference number: 154515; MUID:94011089
 A:Accession: I54515
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-31 <RES>
 A:Cross-references: GR:I02326; NID:g292400; PTDN:AAA16174.1; PID:g451281

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A:Gene: GDB:IGLL2
A:Cross-references: GDB:I37325
A:Map position: 22q11.2-22q11.2
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match          14.2%; Score 43; DB 2; Length 31;
Best Local Similarity 37.5%; Pred. NO. 3.8e+02;
Matches 9; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 32 EPSTAPSTSFLLPMGPPAEGST 55
      :| | | | | | | | | |
Db 2 QPKTTPSVILFLPSCEEPQANKAT 25

RESULT 13

```

collagen alpha 2(V) chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-1995
C:Accession: A45662

R;Mayne, R.; Brexton, R.G.; Mayne, P.M.; Baker, J.R.

J. Biol. Chem. 288, 9381-9386, 1993

A;Title: Isolation and characterization of the chains of type V/type XI collagen present

A;Reference number: A46662; MUID:93252802

A;Accession: A46662

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-39 <MAY>

A;Experimental source: vitreous humor

A;Note: sequence extracted from NCBI backbone (NCBIP:131547)

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Search completed: February 12, 2002, 13:00:37

Job time: 112 sec

Query Match 14.2%; Score 43; DB 2; Length 39;

Best Local Similarity 53.3%; Pred. No. 4.8e+02;

Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 43 LPMGPPPPAEGSTGD 57

Db 14 LPGPPPPGAGPGD 28

RESULT 14

A37172

collagen alpha 1(XII) chain-like, skin and tendon - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 19-Oct-1995

C;Accession: A37172

R;Dublet, B.; Van Der Rest, M.

Ann. N. Y. Acad. Sci. 580, 436-439, 1989

A;Title: Comparison between chicken type XII collagen and bovine homologues.

A;Reference number: A37172

A;Accession: A37172

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-36 <DUB>

Query Match 13.9%; Score 42; DB 2; Length 36;

Best Local Similarity 41.4%; Pred. No. 5.4e+02;

Matches 12; Conservative 3; Mismatches 8; Indels 6; Gaps 3;

QY 25 QHTQPTPEPSTA-PSTSFLLPMGPPPAE 52

Db 3 QERSP-PQANAVPSX----PASPSPLQ 26

RESULT 15

I46522

troponin T 2fa - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999

C;Accession: I46522

R;Briggs, M.M.; Lin, J.J.; Schachat, F.H.

J. Muscle Res. Cell. Motil. 8, 1-12, 1987

A;Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle tropo

A;Reference number: I46522; MUID:87251333

A;Accession: I46522

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-48 <BRI>

A;Cross-references: EMBL:U04975; NID:g440810; PIDN:AAA16028.1; PID:g440811

C;Superfamily: troponin T

Query Match 13.9%; Score 42; DB 2; Length 48;

Best Local Similarity 37.9%; Pred. No. 7.3e+02;

Matches 11; Conservative 3; Mismatches 9; Indels 6; Gaps 2;

QY 10: APCAVALPQVPVRSQHTQTPPS-TAP 37

Db 25 SPAEVEPEPV-----HEEEKPRKLTAP 48

OX NCBI_

RT "The complete nucleotide sequence of Japanese flounder mitochondrial
 RT genome: structural property and cue for resolving teleostean
 RT relationship.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
 CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
 CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
 CC -----
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 CC -----
 DR EMBL; AB028664; BAA89037.1; -;
 DR InterPro; IPR001421; ATP-synt_8.
 DR Pfam; PF00895; ATP-synt_8; 1.
 DR KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 SQ SEQUENCE 55 AA; 6571 MW; 2B5EFE20FDCB6AA9 CRC64;

Query Match. 12.6%; Score 38; DB 1; Length 55;
 Best Local Similarity 29.2%; Pred. No. 1.2e+03;
 Matches 7; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 16 LPQVSTRSQHTQTPPESTAPST 39
 Db 24 IPPKVLATFPNEPTQSTQPKT 47
 :| | : :| | : | |

RESULT 9
 FOR2_MYRGU STANDARD; PRT; 16 AA.
 ID P81437;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE FORMACIN 2.
 OS Myrmecia gulosa (Red bulldog ant).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Formicidae; Myrmecinae; Myrmecia.
 OX NCBI_TaxID=36170;
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
 RC TISSUE=Hemolymph;
 RX MEDLINE=98165787; PubMed=9497332;
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
 RT "Isolation from an ant Myrmecia gulosa of two inducible
 RT O-glycosylated proline-rich antibacterial peptides.";
 RL J. Biol. Chem. 273:6139-6143(1998).
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
 CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
 CC BACTERIA.
 CC -!- INDUCTION: UPON BACTERIAL CHALLENGE.
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
 CC Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 KW CARBOHYD 11 11 O-LINKED (GALNAC...);
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3H00BC2E0AE CRC64;

Query Match. 12.4%; Score 37.5; DB 1; Length 16;
 Best Local Similarity 47.1%; Pred. No. 4e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy 17 PQPVSTRSQHTQTPPEP 33
 Db 3 PNPVNTK-----PTYP 14
 :| | : | | |

RESULT 10
 RPOK_HALMA STANDARD; PRT; 57 AA.
 ID P29200;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
 GN RPOK.
 OS Haloarcula marismortui (Halo bacterium marismortui).
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.
 OX NCBI_TaxID=2238;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92105119; PubMed=1840597;
 RA Kroemer W.J., Arndt E.;
 RT "Halobacterial S9 operon. Three ribosomal protein genes are
 RT cotranscribed with genes encoding a tRNA(Leu), the enolase, and a
 RT putative membrane protein in the archaeobacterium Haloarcula
 RT (Halobacterium) marismortui.";
 RL J. Biol. Chem. 266:24573-24579(1991).
 RN [2]
 RP SIMILARITY.
 RX MEDLINE=94321350; PubMed=8045907;
 RA McKune K., Woychik N.A.;
 RT "Halobacterial S9 operon contains two genes encoding proteins
 RT homologous to subunits shared by eukaryotic RNA polymerases I, II,
 RT and III.";
 RL J. Bacteriol. 176:4754-4756(1994).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE -> N PYROPHOSPHATE +
 CC RNA(N).
 CC -!- SIMILARITY: BELONGS TO THE ARCHAEABACTERIA RPOK / EUKARYOTIC RPB6
 CC RNA POLYMERASE SUBUNIT FAMILY.
 CC -----
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 CC -----
 DR EMBL; M76567; AAA73100.1; -;
 DR PIR; E41715; E41715.
 DR InterPro; IPR001725; RNA_polK_14KD.
 DR Pfam; PF01192; RNA_pol_K; 1.
 DR PROSITE; PS0111; RNA_POL_K_14KD; 1.
 KW Transferase; DNA-directed RNA polymerase; Transcription.
 SQ SEQUENCE 57 AA; 6291 MW; D299FDA1954D030F CRC64;

Query Match. 12.4%; Score 37.5; DB 1; Length 57;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 9; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

Qy 9 MAPGAVHLPPQVSTRSQHTOP 29
 Db 21 LAHGA-----PVLIEHTOP 36
 :| | | | :| | | |

RESULT 11
 YPU3_RHOCA STANDARD; PRT; 55 AA.
 ID YPU3_RHOCA
 AC P26159;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE HYPOTHETICAL 5.8 KDA PROTEIN IN PUHA 5'REGION (ORF55).

OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]

RP BURKE D.H., Alberti M., Armstrong G.A., Hearst J.E.;
RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----

DR EMBL; Z11165; CAA77517.1; .
DR PIR; S17805; S17805.
KW Photosynthesis; Hypothetical protein.
SQ SEQUENCE 55 AA; 5750 MW; 7EB55296266D48B1 CRC64;

Query Match 12.1%; Score 36.5; DB 1; Length 55;
Best Local Similarity 40.5%; Pred. No. 1.6e+03;
Matches 15; Conservative 2; Mismatches 17; Indels 3; Gaps 2;

QY 18 QPVSTRSQHTQPTPEPS--TAPSTSFLLPMGSP-PA 51
: | | | | | | | | : | | | | |
Db 9 RPSAAPARQPCGSCVTAPVAVRIGAMGASPGPA 45

RESULT 12

AP65_CARMA STANDARD; PRT; 30 AA.
AC P82964;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTIBACTERIAL 6.5 KDA PROTEIN (FRAGMENT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]

SEQUENCE, AND FUNCTION.

RC TISSUE=HEMOCYTE;
RX MEDLINE=97008941; PubMed=8856051;
RA Schnapp D., Kemp G.D., Smith V.J.;
RT "Purification and characterization of a proline-rich antibacterial
RT peptide, with sequence similarity to bactericin-7, from the haemocytes
RT of the shore crab, Carcinus maenas".
RL Eur. J. Biochem. 240:532-539(1996).
CC -!- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST P. IMMOBILIS AND
CC M. LUTEUS, LESS ACTIVE AGAINST E. COLI D22.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW IS: 6.5 KDA.
CC -!- SIMILARITY: TO BOVINE BACTENECIN 7.
KW Antibiotic.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3305 MW; 6E2C2205934896C4 CRC64;

Query Match 11.9%; Score 36; DB 1; Length 30;
Best Local Similarity 38.1%; Pred. No. 9.8e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 6; Gaps 1;

QY 29 PTPEPSTAPSTSFLLPMGSP 49
: | | | | | | | | : | | | | |
Db 4 PYRPPRP-----PIGPRP 18

RESULT 13

REVISONS.

ATP8_SQUAC STANDARD; PRT; 55 AA.
ID Q9Z250;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
GN ATP8 OR ATP8.
OS Squalus acanthias (Spiny dogfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99091711; PubMed=9873084;
RA Rasmussen A.S., Arnason U.;
RT "Phylogenetic studies of complete mitochondrial DNA molecules place
RT cartilaginous fishes within the tree of bony fishes.";
RL J. Mol. Evol. 48:118-123(1999).
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y18134; CAA77053.1; .
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8_1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 6 26 POTENTIAL.
SQ SEQUENCE 55 AA; 6587 MW; 3FB9F843CEFA54EE CRC64;

Query Match 11.9%; Score 36; DB 1; Length 55;
Best Local Similarity 35.3%; Pred. No. 1.7e+03;
Matches 12; Conservative 2; Mismatches 12; Indels 8; Gaps 1;

QY 14 VHLPPQVSTRSQHTQPT-----PEPSTAPST 39
: | | | | | | | | : | | | | |
Db 22 VILPKKVMTHLFNNPTAKSAEKPKPEPWNWPT 55

RESULT 14
INEL_HUMAN STANDARD; PRT; 51 AA.
ID INEL_HUMAN
AC O15225;
DT 15-JUL-1999 (Rel. 38, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE INACTIVATION ESCAPE 1 PROTEIN (DXS6974E).
GN INEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97386586; PubMed=9244435;
RA Esposito T., Gianfrancesco F., Ciccodicola A., D'Esposito M.,
RA Nagaraja R., Mazzarella R., D'Urso M., Forabosco A.;
RT "Escape from X inactivation of two new genes associated with DXS6974E
RT and DXS7020E.";
RL Genomics 43:183-190(1997).
RN [2]
RP REVISONS.

Forabosco A.;
Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PANCREAS, HEART AND LIVER
FOLLOWED BY BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
MOSTLY EXPRESSED IN FEMALES.

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EMBL; Y10696; CAA71702.2; -
MDM; 300164; -
SEQUENCE 51 AA: 5425 MW: 6F59QC65E8BDBAD CRC64:
SQ

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	60.5	20.0	52	4	Q14441	Q14441	homo sapien
2	55.5	18.4	42	4	Q15469	Q15469	homo sapien
3	52	17.2	52	12	Q92313	Q92313	human resp
4	51	16.9	52	12	Q92301	Q92301	human resp
5	51	16.9	52	12	Q92314	Q92314	human resp
6	50.5	16.7	33	6	Q02832	Q02832	gorilla gor
7	50.5	16.7	54	11	Q9WT77	Q9WT77	mus musculus
8	50	16.6	52	6	Q9GL38	Q9GL38	bos taurus
9	49.5	16.4	54	12	Q9J7C8	Q9J7C8	simian vire
10	49	16.2	46	4	Q15218	Q15218	homo sapien
11	49	16.2	51	6	Q18723	Q18723	macaca fusc
12	49	16.2	52	12	Q92302	Q92302	human resp
13	49	16.2	52	12	Q92303	Q92303	human resp
14	48	15.9	38	4	Q9HB17	Q9HB17	homo sapien
15	48	15.9	42	6	Q9CKJ3	Q9CKJ3	sus scrofa
16	47.5	15.7	27	10	Q9S8M0	Q9S8M0	solanum tub
17	47.5	15.7	57	4	Q13697	Q13697	homo sapien
18	47.5	15.7	5	9	Q9VQ06	Q9VQ06	drosofila
19	47	15.6	31	2	Q9Z516	Q9Z516	strepomyce

```

OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=181691;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic Variability among Group A and Group B Respiratory Syncytial
RL Viruses in a Children's Hospital.";
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF086872; AAC42992.1; -
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT 52
SQ SEQUENCE 52 AA; 5613 MW; 7C3114ACA02574E6 CRC64;

Query Match 16.9%; Score 51; DB 12; Length 52;
Best Local Similarity 34.3%; Pred. No. 73; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 19;

QY 15 HLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
| | | | | | | | | | | | | | | | | | | |
DB 13 HTSQKETHSTSEGNPSQSVYTTSEYLSQSPSP 47
| | | | | | | | | | | | | | | | | | | |

RESULT 5
O92314 PRELIMINARY; PRT; 52 AA.
AC O92314;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=203721;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic Variability among Group A and Group B Respiratory Syncytial
RL Viruses in a Children's Hospital.";
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF086888; AAC43008.1; -
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT 52
SQ SEQUENCE 52 AA; 5554 MW; 3B328FBC5B4E9858 CRC64;

Query Match 16.9%; Score 51; DB 12; Length 52;
Best Local Similarity 31.8%; Pred. No. 73;
Matches 14; Conservative 5; Mismatches 25; Indels 0; Gaps 0;

QY 6 TRSMAPCAVHLPOPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
| | | | | | | | | | | | | | | | | | | |
DB 4 TNSITGNLEHTSQEETHSTSEGNTPSQSVYTTSEYLSQSPSP 47
| | | | | | | | | | | | | | | | | | | |

RESULT 6
O02832 PRELIMINARY; PRT; 33 AA.
AC O02832;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HUNTINGIN PROTEIN (FRAGMENT).
GN IT15.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla

```

OX NCBI_TaxID=9595;

RN SEQUENCE FROM N.A.
RP MEDLINE=96326790; PubMed=8766138;
RX Pecheux C., Gail A.L., Kaplan J.C., Dode C.;
RA "Sequence analysis of the CAG triplet repeats region in the Huntington
RT disease gene (hrl5) in several mammalian species.";
RL Ann. Genet. 39:81-86(1996).
DR EMBL; S83377; AAB50771.1; -.
FT NON_TER 1
SQ SEQUENCE 33 AA; 3393 MW; 44F58CE5636722A CRC64;

Query Match 16.7%; Score 50.5; DB 6; Length 33;

Best Local Similarity 38.5%; Pred. No. 54;

Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 3;

QY 16 LPQVSTRSQHTQ-TPEPSTAPSTSELLPMGPSPPAEG 53

Db 2 LPQP-----PPHGQPLLPOQPQP-----PPPPPPPPPG 30

RESULT 7

Q9WTY7 ID Q9WTY7 PRELIMINARY; PRT; 54 AA.

AC Q9WTY7; 54 AA.

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).

GN NOS3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV129;

RX MEDLINE=99096466; PubMed=9878824;

RA Teichert A.M., Karantzoulis-Pegaras F., Wang Y., Mawji I.A., Bei X.,

RA Gnanapandithen K., Marsden P.A.;

RT "Characterization of the murine endothelial nitric oxide synthase

RT promoter.";

RL Biochim. Biophys. Acta 1443:352-357(1998).

DR EMBL; AF091262; AAD22613.1; -.

FT NON_TER 54

SQ SEQUENCE 54 AA; 5193 MW; 1DA456A21958B2EA CRC64;

Query Match

Best Local Similarity 47.8%; Score 50.5; DB 11; Length 54;

Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 1;

QY 29 PTEPSTAPSTSELLPMGPSPPA 51

Db 34 PAPEPSQA-----PPSPTRPA 51

RESULT 8

Q9GL38 ID Q9GL38 PRELIMINARY; PRT; 52 AA.

AC Q9GL38; 52 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE CALPASTATIN (FRAGMENT).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV129;

RX MEDLINE=99096466; PubMed=9878824;

RA Teichert A.M., Karantzoulis-Pegaras F., Wang Y., Mawji I.A., Bei X.,

RA Gnanapandithen K., Marsden P.A.;

RT "Characterization of the murine endothelial nitric oxide synthase

RA Chung H.Y., Davis M.E., Hines H.C.;

RT "PCR-SSCP analysis of the bovine calpastatin gene domain L region.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

FT EMBL; AY008267; AAG23869.1; -.

FT NON_TER 1

FT NON_TER 52

SQ SEQUENCE 52 AA; 5749 MW; CBD5A7449AFDDA89 CRC64;

Query Match 16.6%; Score 50; DB 6; Length 52;

Best Local Similarity 33.3%; Pred. No. 94;

Matches 11; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 5 PTRMAPGAVHLPQPVSTRSQHTQTPPEPSTAP 37

Db 19 PKHSDTGTGSHAPKEKAVSKSSEQPPSEKSTKP 51

RESULT 9

Q9J7C8 ID Q9J7C8 PRELIMINARY; PRT; 54 AA.

AC Q9J7C8; 54 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE LARGE T ANTIGEN (FRAGMENT).

OS Simian virus 40 (SV40).

OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

OX NCBI_TaxID=10633;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MC-028863B-1;

RA Rizzo P., Carbone M.;

RT "SV40 from 1955 commercial parenteral (Salk) poliovaccine.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF180738; AAF28272.1; -.

FT NON_TER 1

SQ SEQUENCE 54 AA; 5868 MW; 556CDAB682C1EFCD CRC64;

Query Match

Best Local Similarity 32.7%; Score 49.5; DB 12; Length 54;

Matches 16; Conservative 5; Mismatches 25; Indels 3; Gaps 2;

QY 8 SNAPGAVHLPQPVSTRSQHTQTPPEPSTAPSTSELLPMGPSPPAEGST 55

Db 8 SOSQSGFQAPQPSQSSQSHDHNPYHICRGXTCXKKP--PTPPPPPET 54

RESULT 10

Q15218 ID Q15218 PRELIMINARY; PRT; 46 AA.

AC Q15218; 46 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)

DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)

DE SALIVARY PROLINE-RICH PROTEIN 2 (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=84298176; PubMed=6089212;

RA Azen E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,

RA Maeda N., Vanin E.F., Carlson D.M., Smithies O.;

RT "Clones from the human gene complex coding for salivary proline-rich

RT proteins";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5561-5565(1984).

DR EMBL; K02578; AAA36505.1; -.

FT NON_TER 1

FT NON_TER 46

SQ SEQUENCE 46 AA; 4592 MW; FCEID38D8DEDC173 CRC64;

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DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5530 MW; C2029E4C5B551270 CRC64;

Query Match 16.2%; Score 49; DB 4; Length 46;
Best Local Similarity 38.2%; Pred. No. 1.1e+02;
Matches 13; Conservative 2; Mismatches 15; Indels 4; Gaps 1;

Qy 21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPAEGS 54
Db 1 SARS-----PPRKPOGPOEGNNGPPPPAGGN 30

RESULT 11
O18723 PRELIMINARY; PRT; 51 AA.
AC O18723;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE COMPLEMENT DEAC-ACCELERATING FACTOR (CD55) (FRAGMENT).
GN DAF.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=98099759; PubMed=9435343;
RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;
RT "A new repetitive sequence uniquely present in the decay-accelerating
RT factor genes.";
RL Immunogenetics 47:246-255(1998).
CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
CC -1- SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
CC (RCA) FAMILY.
CC EMBL; AB003315; BAA22903.1; -.
DR Complement pathway.
KW NON_TER 1
FT NON_TER 51
FT NON_TER 51
SQ SEQUENCE 51 AA; 5545 MW; ED112B05C37548A6 CRC64;

Query Match 16.2%; Score 49; DB 6; Length 51;
Best Local Similarity 28.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

Qy 11 PGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPAEGST 55
Db 3 PPTVQKPTTVNRTEVSPSTQKITTPNAQ---ATRTSPASRTT 43

RESULT 12
O92302 PRELIMINARY; PRT; 52 AA.
AC O92302;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=182473;
RA Coggin W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic Variability among Group A and Group B Respiratory Syncytial
RT Viruses in a Children's Hospital.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF086873; AAC42993.1; -.
DR
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DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5530 MW; C2029E4C5B551270 CRC64;

Query Match 16.2%; Score 49; DB 12; Length 52;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 26; Indels 0; Gaps 0;

Qy 6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
Db 4 TNSTTGNLEHTSQEETLHSTSEGNTPSQAVTTSEYLSQPPSP 47

RESULT 13
O92303 PRELIMINARY; PRT; 52 AA.
AC O92303;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=182701;
RA Coggin W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic Variability among Group A and Group B Respiratory Syncytial
RT Viruses in a Children's Hospital.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF086874; AAC42994.1; -.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT NON_TER 52
FT NON_TER 52
SQ SEQUENCE 52 AA; 5542 MW; C2028FBC5B551270 CRC64;

Query Match 16.2%; Score 49; DB 12; Length 52;
Best Local Similarity 31.8%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 26; Indels 0; Gaps 0;

Qy 6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
Db 4 TNSTTGNLEHTSQEETLHSTSEGNTPSQAVTTSEYLSQPPSP 47

RESULT 14
O9HB17 PRELIMINARY; PRT; 38 AA.
AC O9HB17;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SIGNALING MOLECULE SPECI BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pirone D.M., Fukiara S., Gutkind S.J., Burbelo P.D.;
RT "SPECS, small binding proteins for CDC42 proteins.";
RL J. Biol. Chem. 0:0-0(2000).
DR EMBL; AF286592; AAG17723.1; -.
DR InterPro: IPR001230; Prenyltn.
DR Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
DR EMBL; AF086873; AAC42993.1; -.
DR SEQUENCE 38 AA; 4245 MW; 3B416F3C5ADF4E91 CRC64;
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Query Match 15.9%; Score 48; DB 4; Length 38;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 6; Indels 8; Gaps 2;

QY 14 VHLPPQVSTRSQHTQTPSTAPSTSFLL 43
| | | | | : | : | |
Db 13 VEPQPVSL-----PTPHFN--PKSQLL 34

RESULT 15
Q9GKJ3 PRELIMINARY; PRT; 42 AA.
AC Q9GKJ3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
GN MYLK.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Van Poucke M., Verle M., Tuggle C., Chardon P., Van Zeveren A.,
RA Peelman L.J.;
RT "Integration of porcine chromosome 13 maps."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222917; AAC41130.1; -
KW Kinase.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4677 MW; 78BDD867E66EF64F CRC64;

Query Match 15.9%; Score 48; DB 6; Length 42;
Best Local Similarity 36.6%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 14; Indels 10; Gaps 2;

QY 14 VHLPPQVSTRS---QHTQTPSTAPSTSFLLPMGSPSP 50
| | | | | : | | | | | : |
Db 8 VHSPPQVDFRSVLAKGKTPKTPVPEKLP-----PPKPTTP 42

Search completed: February 12, 2002, 13:03:05
Job time: 185 sec